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September 24, 2004, 14:02:27; Search time 51.308 Seconds (without alignments) 699.375 Million cell updates/sec
                                                                                                                                                                                                             US-10-661-784-3
687
I GSGKDFVQPPTKICVGCPRD......VPWEKKIYPTVTVNHWECEF 127
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                            Sequence:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1

A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

		d			SUMMARIES	
Result No.	Sco	äg.	Length	DB		Description
	618	90.0	123		AAY95426	Aay95426 Human hig
N	н	0.06	304	ω	ABP70801	Abp70801 Human ext
m	618	90.0	322	w	ABP70799	Human
4	н	0.06	329	9	ABU92044	Abu92044 Human pro
'n	618	0.06	358	9	ABP70800	_
9	618	90.0	390	9	ABU99149	Novel
7	m	90.0	300	9	ABU99143	Abu99143 Novel hum
80	ч	0.06	427	ω	ADE76864	4
6	н	90.0	615	9	ABU99144	44 Novel
10	Н	0.06	626	Ŋ	ABB78707	Human
11	\leftarrow	0.06	v	4	ABG21101	Abg21101 Novel hum
12	-	90.0	9	Ŋ	ABB78710	
13	Н	90.0	Ψ	9	ABU99150	Abu99150 Novel hum
14	ᆸ	90.0	Ψ	φ	ABU99145	Novel
15	α	85.3	М	ო	AAB37447	
	585	85.2	4	4	ABG21105	Abg21105 Novel hum
17	•	81.0	-	N	AAR33350	
	4	64.0	4	,	AAP40257	
10	н	60.1	4	Н	AAP40633	Bradyk
	411	59.8	6.3	9	ABR41202	Human
	388	56.5	235	Ŋ	ABG60077	Abg60077 Human DIT
		ė	248	4	ABG21102	Novel
	31	ġ	369	4	ABG21099	Abg21099 Novel hum
	190	27.7	305	4	ABG21100	Novel
	•	•	167	~	AAW98907	Aaw98907 Mouse IMC

-	Aab37445 Human cys	Aaw32323 Mature hu	Aaw31902 Human cys	Aay25708 Human cys	Aae02410 Human cys	Aae04439 Human cys	Add14098 Human src	Aay02287 Secreted	Ada45154 Human pol		Aay95408 Anti-angi	Aab37446 Human kin	Aaw98910 Mouse IMC	Aay95425 Anti-angi	Aay81200 Human mut	Aay81189 Human mut	Aay81198 Human mut	Aay81187 Human mut	Aay81218 Bovine mu	
AAY95418	AAB37445	AAW32323	AAW31902	AAY25708	AAE02410	AAE04439	ADD14098	AAY02287	ADA45154	AAW69734	AAY95408	AAB37446	AAW98910	AAY95425	AAY81200	AAY81189	AAY81198	AAY81187	AAY81218 .	
32 3	126 3	145 2	145 2	145 2	145 4	145 4	145 7	167 2	167 7	178 2	32 3	122 3	167 2	27 3	121 3	128 3	121 3	128 3	118 3	
24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.7	23.7	23.4	22.9	22.5	22.3	21.0	21.0	20.9	20.9	20.7	
166	163.5	163.5	163.5	163.5	163.5	163.5	163.5	163.5	163	163	161	157	154.5	153	144.5	144.5	143.5	143.5	142.5	
26	27	28	29	30	31	3.5	33	3.4	100	9	3.7	. cc	6	4 0	41	42	4	4 4	45	

ALIGNMENTS

RESULT 1

Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3 Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide. Human high mol.wt. kininogen domain 3. AAY95426 standard; peptide; 123 AA 98US-0112427P. 99WO-US028465. 25-SEP-2000 (first entry) (UTEM) UNIV TEMPLE. (MCCR/) MCCRAE R K. WPI; 2000-442247/38 WO200035407-A2. Homo sapiens. 02-DEC-1999; 16-DEC-1998; 22-JUN-2000 Mccrae RK; AAY95426; AAY95426

analog

Disclosure, Page 4; 44pp; English

The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention provides peptides (see AAY95405-24) that are analogues of certain sites in the HX domain 3, specifically ABA75-195282, Cy5246-Cy5249, Leu31-Ty7338 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting anglogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer,

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Sequence 304 AA;
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immunosuppressive, autoimmune disorder; inflammatory disorder; diabetes;
endocrine disorder; cancer.
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on AD, Jin P, Hawkins PR, Tang YT, Burford N;
SD, Tran UK, Chien D, Zebarjadian Y,
3, Chang H, Swarnakar A, Lehr-Mason PM;
                                                                                                                                                                                                                                                                                                                             1 GKDFVQPPTKICVGCPRDIPTNSPELBETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                     3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                               63 AGKKYPIDPVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 116
                                                                                                                                                                                                                         .;
0
                                                                                                                                                              Length 123;
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                                                                                                                                                       90.0%; Score 618; DB 3; I
100.0%; Pred. No. 5.5e-63;
ive 0; Mismatches 0;
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Khare R, Wilson AD,
Yao MG, Becha SD, Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2001; 2001US-0314811P.
14-DEC-2001; 2001US-0340584P.
18-JAN-2002; 2002US-0350595P.
11-MAR-2002; 2002US-0363432P.
15-WAR-2002; 2002US-0364607P.
05-APR-2002; 2002US-0364607P.
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Richardson TW, Kable AE,
                                                                                                                                                                                                                      116; Conservative
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 116; Conserv
                                                                                               Sequence 123 AA;
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Lee SY,
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ABP70801
ABP70801
ACC ABP
XXX ABP70801
ACC ABP ACC ABP
XXX ABP70801
ACC ABP70801
ABP70801
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ACC ABP70
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                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human extracellular messenger (EXMES) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional EXMES e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel human extracellular messenger proteins (EXMES-1 to-28, ABP7074-ABP70801) and their coding sequences (ACC42361-ACC42388). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overtexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elliott VS;
YT, Burford N;
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immunosuppressive, autoimmune disorder, inflammatory disorder, diabetes,
                                                                  GKDFVQPPTKI CVGCPRDI PTNSPELEETLTHTI TKLNAENNATFYFKI DNVKKARVQVV
                                                                                                                                                                 245
                                                                                                                                 63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                   Gaps
                                                                                                                                                    Jin P, Hawkins PR, Tang YT, Burran UK, Chien D, Zebarjadian Y, ng H, Swarnakar A, Lehr-Mason PM;
                                   ;
     Length 304;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walia NK,
   90.0%; Score 618; DB 6;
100.0%; Pred. No. 1.9e-62;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                             Human extracellular messenger, EXMES-26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uggan BM, Lee S, Baughn MR, Hafa
e SY, Khare R, Wilson AD, Jin F
ing L, Yao MG, Becha SD, Tran UK
ichardson TW, Kable AE, Chang H,
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                                                                                                                                                                                                                                            ABP70799 standard; protein; 322
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11-MAR-2002; 2002US-0363432P.
15-MAR-2002; 2002US-0364607P.
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14-DEC-2001; 2001US-0340584P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                            endocrine disorder; cancer,
                                                                                                                                                                                                                                                                                                             (first entry)
Query Match
Best Local Similarity 100.
Matches 116; Conservative
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Sequence 322 AA;

polynucleotides. The diseases or conditions associated with decreased expression or overexpression of PMMM are cell proliferation disorders (e.g. cancer, altherosclerosis), meurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointesinal or epithelial disorders, and infections. The PMMM polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in altering the expression of the target, polymucleotide and compounds specifically bind to, or modulate the activity of the polypeptide. ABU92021-ABU92060 represent the human PMMM polypeptides of the invention

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Gaps .. 0

Length 329;

Sequence 329 AA;

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                                                                                                                                                             GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFVFKIDNVXKARVQVV 207
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Duggan BM, Lee EA, Griffin JA, Li JX;
AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue H;
Richardson TW, Tang TY, Jin P, Chien D;
D, Lee S, Blake JJ, Ho A, Zheng W;
                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; protein modification and maintenance molecule; PWMW; cancer; cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; inflammatory disorder; AIDS; developmental disorder; hypothyroidism; Cushing's syndrome; gastrointestinal disorder; hypothyroidism; infection; cytostatic, antiareriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic.
                                                                                                                 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                  63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                           Gaps
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Length 322;
                                                        0; Indels
90.0%; Score 618; DB 6;
100.0%; Pred. No. 2.1e-62;
iive 0; Mismatches 0;
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09-NOV-2001; 2001US-034887P.
28-NOV-2001; 2001US-033145P.
06-DEC-2001; 2001US-03405P.
14-DEC-2001; 2001US-0340584P.
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Sprague WW, Hafalia AJA
                                  Local Similarity 100.
nes 116; Conservative
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Bhatia U, Burrill JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramkumar J, Gorventry, Becha SD,
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New human extracellular messenger (EXMES) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional EXMES e.g. autoimmune disorders or cancer.
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immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
endocrine disorder; cancer.
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                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS;
Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford
Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y;
on TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;
                                                     3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHT1TKLNAENNATFYFKIDNVKKARVQVV
                                                                         155 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                               63 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                               215 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 270
90.0%; Score 618; DB 6; Length 32 100.0%; Pred. No. 2.2e-62; iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Human extracellular messenger, EXMES-27.
                                                                                                                                                                                                                    ABP70800 standard; protein; 358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , 2001US-0314811P.
2001US-0340564F.
2002US-0350595P.
2002US-0363422P.
2002US-03644607P.
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Ding L, Yao MG, Becha SD,
Richardson TW, Kable AE,
                                                                                                                                                                                                                                                                              (first entry)
    Query Match
Best Local Similarity 100.
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-2001;
18-JAN-2002;
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05-APR-2002;
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The present invention relates to the isolation of human protein modification and maintenance molecules (PMMM), and the polynucleotide sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM—1to PMMM—40) are disclosed. The sequences of the invention are useful for diagnosing a condition or disease associated with the expression of PMMM in a subject, preparing a polyclonal or monoclonal antibody, and generating an expression profile of a sample containing the

New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or

WPI; 2003-430274/40. N-PSDB; ACA92439.

Claim 1; Page 264-265; 311pp; English.

infections.

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The present invention relates to novel human extracellular messenger proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences (ACC42361-ACC42380). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or
                                                                                                                                                                                                                                                  3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, G-protein coupled receptor related protein, GPCR related protein, NOV, cytostatic; cardiant; antiarteriosclerotic; antidiabetic; immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; antiparkinsonian; neuroprotectic; antiasthmatic; haemostatic; antiparkinsonian; neuroprotective; noorropic; gene therapy; vaccine; NOVX-associated disorder; AIDS; obesity; asthmatic; namen disorder; AIDS; obesity; asthmatic; haematopoietic disorder; Parkinson's disease; Alzheimer's disease; haematopoietic disorder; Parkinson's disease; Alzheimer's disease; usurgenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
                                                                                                                                                                                                                                                                                                               AGKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                                                                    244 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 299
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                       90.0%; Score 618; DB 6; Length 358; 100.0%; Pred. No. 2.4e-62; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human GPCR related protein NOV12g.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABU99149 standard; protein; 390 AA
Claim 1; Page 206; 224pp; English.
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2001US-0296404P.
2001US-0296418P.
2001US-029858P.
2001US-029949P.
2001US-0300883P.
2001US-0300883P.
2001US-0300883P.
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                                                                                                                                                                                                    Best Local Similarity 100.
Matches 116; Conservative
                                                                                                                                                          Sequence 358 AA;
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28-JUN-2001;
13-AUG-2001;
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                                                                                                                            cancer
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2002US-0363676P

12-MAR-2002;

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The invention describes an isolated polypeptide (I) comprising any of 27 mature form of them, as dequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a speciated with a human disease selected from a pathology associated with a human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX associated discates, allows associated discates, allows associated discates, allows, asthma, haematopoietic disorders, Parkinson's disease, Alzhahmer's disease, infections, multiple sclerosis, cancer. C discates and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, continuous that haling and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as thybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as varing the amino acid squence of a novel human G-protein complete related protein NOV
                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 GKDFVQPPTKICVGCPRDIPTINSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 275
                                                                                                                 Li L;
                                                                                                                                                             Vernet CAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, G-protein coupled receptor related protein, GPCR related protein, NOV; cytostatic; cardiant; antiarteriosclerotic; antidiabetic; immunomodulator; anti-HIV; ancetic; antiasthmatic; haemostatic; anti-HIV; ancetic; antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;
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                                                                                      Boldog FL, Casman SJ, Edinger SR, nan L, Guo X, Hjalt T, Kekuda R, Li Millet I, Padigaru M, Patturajan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                             Spytek KA,
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                                                                                   Baumgartner JC, Boldog FL, Casma
Gerlach VL, Gorman L, Guo X, Hj
, Malyankar UM, Millet I, Padiga
stelli L, Shimkets RA, Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human GPCR related protein NOV12a.
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 147; 332pp; English.
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03-JUN-2002; 2002US-00363676.
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Matches 116; Conservative
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                                                                                             Ander Gangolli EA, com Gangolli EA, Malyar Macdougall JR, Malyar Rastelli I
                                            (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                          pharmacogenomics
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                                                                                        Anderson DW,
                                                                                                                                                           Pena CEA,
Voss EZ, 1
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haematopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; wasting disorder; chronic disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; andiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

Homo sapiens.

12-DEC-2002.

04-JUN-2002; 2002WO-US017428

04-UN-2001; 20010S-0295601P.
06-JUN-2001; 2001US-02956404P.
06-JUN-2001; 2001US-0296404P.
14-JUN-2001; 2001US-029858P.
15-JUN-2001; 2001US-029856P.
26-JUN-2001; 2001US-0299949P.
26-JUN-2001; 2001US-0301550P.
13-AUG-2001; 2001US-0301550P.
14-SEP-2001; 2001US-031560P.
12-MAR-2002; 2002US-03611B9P.

(CURA-) CURAGEN CORP.

2002US-0363676P 03-JUN-2002; 2002US-00363676 12-MAR-2002;

Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR; Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L; Asdodougall JK, Malyankar UM, Millet I, Padigaru M, Patturajan M; Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CAM; Voss EZ, Zerhusen BD;

WPI; 2003-140627/13.

N-PSDB; ACD03647

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 143; 332pp; English.

The invention describes an isolated polypeptide (I) comprising any of 27 (18-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology syndrome associated with the polypeptide. The NOVX polypeptides, polynuclectides and antibodies are useful in treating or preventing NOVX-associated in an antibodies are useful in treating or preventing NOVX-associated classification, asthma, haematopoletic disorders, parkinson's disorders, AlDS, obesity, asthma, haematopoletic disorders, parkinson's disorders, AlDS, obesity, asthma, haematopoletic disorders, parkinson's disorders, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopolesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in those antibodies that bind immunospecifically to NOVX substances for use in hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as

ö 62 63 ACKYFIDFVARETTCSKESNEBLTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118 3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 284 AGKKYFIDFVARETTCSKESNEELTESCETKKLGGSLDCNAEVYVVPWBKKIYPTV 339 vaccines. This is the amino acid sequence of a novel human G-protein coupled receptor related protein NOV ö Length 398; Indels Pred. No. 2.8e-62; Mismatches 0; 90.0%; Score 618; DB 6; 100.0%; Pred. ... Best Local Similarity 100. Matches 116; Conservative Query Match Best Local Similarity Sequence 398 AA; 셤 88833 ò

RESULT 8 ADE76864

ADE76864 standard; protein; 427 AA

ADE76864;

29-JAN-2004 (first entry)

Human protein expressed in a liver disorder #9.

human, liver disorder, hyperlipidaemia, hypertension, type II diabetes, tumour, liver, inflammatory disorder, immune response disorder, high-throughput screening, differential gene expression, gene therapy.

Homo sapiens.

US2003108871-A1

12-JUN-2003

30-JUL-2001; 2001US-00919039.

28-JUL-2000; 2000US-0222113P.

(KASE/) KASER M R.

Kaser MR;

WPI; 2004-031227/03

N-PSDB; ADE76863

Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver disorders.

Claim 1; SEQ ID NO 29; 41pp; English.

The invention relates to a composition comprising several CDNAs that are differentially expressed in a liver disorder. The composition is useful coff tracting liver disorder such as hyperlipidaemia, hypertension, Eype for treating liver disorder such as hyperlipidaemia, hypertension, Eype II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of several molecules or compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the CDNA with several of molecules or compounds under conditions to allow specific binding between the protein and a compound, therefore identifying a ligand which specifically conditions the protein. The composition is useful for detecting and composition is useful for detecting and community of treatment. The present sequence represents the amino acid sequence of a protein encoded by a CDNA differentially expressed in a

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WO200214369-A2
loss EZ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FL, Casman SJ, Edinger SR;
Guo X, Hjalt T, Kekuda R, Li L;
I, Padigaru M, Patturajan M;
Stone DJ, Spytek KA, Vernet CAM;
                                                                                                                                                                                                                                                                                                                NOV, cytostatic, cardiant; antiarteriosclerotic; antidiabetic; immunomodiator; antidiabetic; immunomodiator; antidiabetic; antiderwinatic; haemostatic; antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine; NoVx-associated disorder; cardiomyopathy; atherosclerosis; cancer; hamme disorder; AIDS; obseity; asthma; haematopoietic disorder; AIDS; obseity; asthma; haematopoietic disorder; Parkinson's disease; Alaheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; wasting disorder; chronic disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenemic.
                                                                                                                                                                                                                                                                                                       Human; G-protein coupled receptor related protein; GPCR related protein;
                                                                                                                                  63 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                              313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 368
                                                                  Gaps
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                                            Length 427;
                                                                Indels
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                                                     100.0%; Pred. No. 3.1e-62; ive 0; Mismatches 0;
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Gangolli EA, Gerlach VL, Gorman L, Guo X, Hj
Macdougall JR, Malyankar LW, Millet I, Padiga
Pena CEA, Rastelli L, Shimkets RA, Stone DJ,
                                           Score 618; DB 8;
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                                                                                                                                                                                                              ABU99144 standard; protein; 615 AA
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2001US-0295661P.
2001US-0296404P.
2001US-0296418P.
2001US-0298285P.
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2001US-029949P.
2001US-0300883P.
2001US-0301550P.
2001US-03115071P.
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14-SEP-2001; 2001US-0322293P.
17-SEP-2001; 2001US-0322706P.
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                                                    Best Local Similarity 100.
Matches 116; Conservative
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                    Sequence 427 AA;
liver disorder.
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26-JUN-2001;
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27-AUG-2001;
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                                           Query Match
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ABU99144
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The invention describes an isolated polypeptide (I) comprising any of 27 [118-96] residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardingnypathy, atherosciercis, cancer, diabetes, immune disorders, AIDS, obesity, asthma, haematopoietic disorders, parkinson's disease, AIDS, obesity, asthma, haematopoietic disorders, parkinson's disease, AIDS, obesity, asthma, manatopoietic disorders, parkinson's disease. AIDS and polypeptides may also be used as targets of the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therappy, in generation of the indimunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein and protein NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                      New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardlomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 GKDFVQPPTKICVGCPRDIPTNSPELEETLITHTITKLNAENNATFYFKIDNVKKARVQVV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, kininogen, high molecular weight kininogen, HK, D5 domain, D5 receptor, angiogenesis, endothelial cell; cytostatic; antitumour; antiatheroscalerctic; vasotropic; vulnerary; tranquilliser; thrombolytic; ophthalmological; gynaecological, antiulcer; antidiabetic; antiathritic; antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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Best Local Similarity 100.0%; Pred. No. 5.1e-62;
Matches 116; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 144; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384. .508
/label= D5_domain
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Zerhusen BD;
                                                                                            WPI: 2003-140627/13.
                                                                                                                                               N-PSDB; ACD03648
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The present invention describes an isolated polypeptide (I) that
corresponds to the D5 domain of human kininogen, or biologically active
peptide fragment, homologue or functional derivative, and which: (a)
inhibite anglogenesis; (b) binds to the D5 binding site on endothablal
cells (EC); (c) activates signalling pathways leading to the introduction
of apoptosis in EC; and/or (d) inhibits the signalling pathway required
for maintenance of EC viability. (l) has cytostatic, antitumour,
antiatherosclerotic, vasorropic, vulnerary, tranquilliser, thrombolytic,
ophthalmological, apraecological, antiuder, antidabetic, antiathritic,
antianglogenic, antiapoptodic and endocrine activities. An antibody (IX)
specific for an epitope of (I) is useful for inhibiting tumour growth or
specific for an epitope of (II) can be used for inhibiting EC
anglogenesis in a subject. (I), a D5 fusion polypeptide (II) or a dimeric
or trimeric fusion polypeptide (III) can be used for inhibiting EC
migration, proliferation, invasion, or anglogenesis, or for inducing EC
apoptosis. An anglogenic EC-targeting pharmaccutical composition (X)
comprising (I), (III), or (IIII), or (III), or (III), or (III), or (III), or (III), or (III), 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation, invasion or angiogenesis. (I), (II), or (III) can be used for isolating a D5 domain binding molecule from a complex mixture and for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the mature human high molecular weight kininogen (HK) protein, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human kininogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 84pp; English.
                                                                                              24-JUL-2001; 2001WO-US023185.
                                                                                                                                                                   24-JUL-2000; 2000US-0220194P.
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Matches 116; Conservative
                                                                                                                                                                                                                                                                                                      Juarez JC;
                                                                                                                                                                                                                                    (ATTE-) ATTENUON LLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperplasia.
                             21-FEB-2002.
                                                                                                                                                                                                                                                                                                      Mazar AP,
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235 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 294 62 3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 350 63 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118 .; 0 90.0%; Score 618; DB 5; Length 626; 100.0%; Pred. No. 5.3e-62; .ive 0; Mismatches 0; Indels 295 g ð à

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312 62

> Novel human diagnostic protein #21092. ABG21101 standard; protein; 644 AA (first entry) 18-FEB-2002 ABG21101; RESULT 11 ABG2110

Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Human, kininogen, high molecular weight kininogen, HK, DS domain, DS receptor, angiogenesis, endothelial cell, cytostatic, antitumour;

Human high molecular weight kininogen (HK) protein.

18-JUL-2002 (first entry)

MAKE KE KAKA

ABB78710;

ABB78710 standard; protein; 644 AA

Homo sapiens

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) exploynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartifying expressed cartifying expressed sequence therapy techniques to restore normal sectivity of (II) or to treat disease states involving (II). (II) is useful in gene in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abservant protein expression or biological activity. The polypeptide and polymuclocide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of dem and products dependent on DNA and amino acid sequences. Asgonolo-Asg30377 represent novel human diagnostic maino acid sequences. Asgonolo-Asg30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at 253 GKDFVQPPTKICVGCPRDIPTNSPBLEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 113 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 368 63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118 0; Gaps New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. Length 644; 90.0%; Score 618; DB 4; Length 64. 100.0%; Pred. No. 5.5e-62; ive 0; Mismatches 0; Indels Claim 20; SEQ ID NO 51460; 103pp; English. 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT Local Similarity 100.0 WPI; 2001-639362/73. N-PSDB; AAS85288. Drmanac RT, Liu C, (HYSE-) HYSEQ INC. Sequence 644 AA; WO200175067-A2 11-0CT-2001 Query Match Matches RESULT 12 ABB78710 à 셤 8

Mon Sep

312 62

253 GKDFVOPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVOVV 3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV

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The present invention describes an isolated polypeptide (I) that

Corresponds to the D5 domain of human kininogen, or biologically active

C peptide fragment, homologue or functional derivative, and which: (a)

inhibits angiogenesis; (b) binds to the D5 binding site on endothelial

CC of apoptoosis in EC; and/or (d) inhibits the signalling pathway required

CC maintenance of EC viability. (I) has cytostatic, antiumour, required

CC antiatherosclerotic, vasotropic, vulnerary, tranquilliser, thrombolytic,

CC antiatherosclerotic, vasotropic, vulnerary, tranquilliser, thrombolytic,

CC antiathological, gynaecological, antiuleer, antidiabetic, antiathkritic,

CC antianglogenic, antiapoptotic and endocrine activities. An antibody (IX)

CC specific for an epitope of (I) is useful for inhibiting tumour growth or

CC angiogenesis in a subject. (I), a D5 fusion polypeptide (II) or a dimeric

CC or trimeric fusion polypeptide (III), and be used for inhibiting EC

angiogenesis. An angiogenic EC-targeting pharmaceutical composition (X)

CC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X)

CC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X)

CC apoptosis. Solating a D5 domain binding molecule from a complex mixture and for

isolating or enriching cells expressing D5 domain binding sites from a

cell mixture. The present sequence represents the human high molecular

CC weight Kininogen (HX) protein, which is given in the exemplification of

the present invention
antiatherosclerotic, vasotropic, vulnerary; tranquilliser, thrombolytic, ophthalmological; gynaecological; antiulcer; antidiabetic, antiarthritic; antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                            mature_human_high_molecular_weight_kininogen
                                                                                                                                                                                                                                      Location/Qualifiers
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/label= signal
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/label= m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-393611/42.
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                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                Peptide
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Human, G-protein coupled receptor related protein, GPCR related protein, NOV; cytostatic; cardiant; antiateriosclerotic; antidiabetic; anti-HIV; anti-HIV; antiasthmatic; haemostatic; anti-HIV; antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; haemacopoietic disorder; AIDS; obesity; asthmather, simune disorder; AIDS; obesity; asthmather, simune disorder; AIDS; obesity; asthmather, simune disorder; cardiomyopathy; atheriars; infection; multiple sclerosis; cancer-associated cachexia; infection; multiple sclerosis; cancer-associated cachexia; cell proliferation; haematopoiesis; wound healing; anglogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FL, Casman SJ, Edinger SR;
Guo X, Hjalt T, Kekuda R, Li L;
I, Padigaru M, Patturajan M;
Stone DJ, Spytek KA, Vernet CAM;
63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV
               313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGGSLDCNAEVYVVPWEKKIYPTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NOVX polypeptides and nucleic acids, useful for preventing or
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
                                                                                                                                                                                            Novel human GPCR related protein NOV12h.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DW, Baumgartner JC, Boldog
Gangolli EA, Gerlach VL, Gorman L,
Macdougall JR, Malyankar UM, Millet
Pena CEA, Rastelli L, Shimkets RA,
Voss EZ, Zerhusen BD;
                                                                                                        ABU99150 standard; protein; 644 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0295607P.
2001US-029561P.
2001US-0296410P.
2001US-0296418P.
2001US-029828P.
2001US-0298556P.
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2001US-0311972P.
2001US-0315071P.
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2001US-0341186P.
2002US-0361189P.
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2002US-0363676P.
2002US-00363676
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                                                                                                                                                                01-AUG-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-140627/13.
N-PSDB; ACD03654.
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21-UW-2001;
26-UW-2001;
28-UW-2001;
27-AUG-2001;
27-AUG-2001;
29-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2001;
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90.0%; Score 618; DB 5; Length 644; ilarity 100.0%; Pred. No. 5.5e-62; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 116; Conservat

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The invention describes an isolated polypeptide (I) comprising any of 27 [18-96] residue amino acid sequences, given in the specification, a manure form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology of syndrome associated with the polypeptide. The NOVX polypeptides, polynuclectides and antibodies are useful in treating or preventing NOVX-associated disorders, AlDS, obesity, asthma, haematopoietic disorders, Parkinson's disease, AlZheimer's disease, infections, multiple sclerosis, cancerses, cancerses, AlZheimer's disease, infections, multiple sclerosis, cancerses, associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and anglogenesis, in gene therappy in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein as coupled receptor related protein NOV
atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
                                                                                        Claim 1; Page 148; 332pp; English.
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253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312 3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 63 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118 313 AGKKYFIDFVARETTCSKESNBELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV·368 0; Gaps 90.0%; Score 618; DB 6; Length 644; 100.0%; Pred. No. 5.5e-62; 0; Indels 100.0%; Pred. w.. Best Local Similarity 100. Matches 116; Conservative Query Match d ð

Sequence 644 AA;

ABU99145 standard; protein; 644 AA. ABU99145; RESULT 14

01-AUG-2003 (first entry)

Novel human GPCR related protein NOV12c.

Human; G-protein coupled receptor related protein; GPCR related protein; NOV; cytostatic; antidiabetic; antidiabetic; antidiabetic; antiparkinsonian; anti-HIV; anorectic; antidiathmatic; haemostatic; antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; diabetes; immune disorder; AIDS; obesity; asthma; haemacopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachaxia; wasting disorder; chromic disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; anglogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

Homo

WO200299116-A2

12-DEC-2002

04-JUN-2002; 2002WO-US017428.

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2001US-0295661P.
2001US-0296404P.
2001US-0298282EP.
2001US-0298256P.
2001US-0299349P.
2001US-03008839P.
2001US-0311972P.
2001US-0311972P.
2001US-0311972P.
2001US-0311972P.
2001US-0311972P.
2001US-03122239.
2001US-03122239.
                                                                                2002US-00363676
        06-JUN-2001;
06-JUN-2001;
14-JUN-2001;
                      15-JUN-2001;
21-JUN-2001;
26-JUN-2001;
                                   28-JUN-2001;
13-AUG-2001;
27-AUG-2001;
                                                 29-AUG-2001;
                                                     14-SEP-2001;
                                                          17-SEP-2001;
                                                                                03-JUN-2002;
                                                                        12-MAR-2002;
                                                                            12-MAR-2002;
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(CURA-) CURAGEN CORP.

Li L; Spytek KA, Vernet CAM; Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR; Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li Macdougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M; Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet C Voss EZ, Zerhusen BD;

WPI; 2003-140627/13. N-PSDB; ACD03649.

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62

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 144-145; 332pp; English.

The invention describes an isolated polypeptide (1) comprising any of 27 (18-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 * dientical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, and carrier, a manufacturing a medicane, cancer. C disorders, Alzheimer's disease, infections, memerapoletic disorders, parkinson's disease. Alzheimer's disease, infections, multiple sclerosis, cancer associated cachexia, and other wasting disorders associated with chronic for the identification of small molypeptides may also be used as targets of murphodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as converted and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein of coupled receptor related protein NOV

Sequence 644 AA;

0; Gaps Length 644; 0; Indels Query Match 90.0%; Score 618; DB 6; L Best Local Similarity 100.0%; Pred. No. 5.5e-62; Matches 116; Conservative 0; Mismatches 0;

3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV

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63 ACKKYFIDFVARETTCSKESNEELFESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118

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The present invention relates to inhibition of the enzymatic activity of legumain or a legumain-related endopeptidase by cystatin. The inhibition involves an interaction between legumain and a papain-non-reactive site of cystatin. Legumain (EC 3.4.2.34) is a cysteine endopeptidase, and performs a protein-processing function. The present sequence is human kininogen D3, which was used in the present invention. Kininogen is a
                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of cystatin.
313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 368
                                                                                                                                                                                    Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
                                                                   AAB37447 standard; protein; 122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 4; 45pp; English.
                                                                                                                                                                                                                                                                                                20-APR-2000; 2000WO-GB001571.
                                                                                                                                                                                                                                                                                                                             99GB-00009133.
                                                                                                                                                                                                                                                                                                                                                                                   Abrahamson M, Barrett AJ;
                                                                                                                                                                                                                                                                                                                                                        (BABR-) BABRAHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687316/67.
                                                                                                                                                      Human kininogen D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 3 cystatin
                                                                                                                                                                                                                                          WO200064945-A1.
                                                                                                                                                                                                                                                                                                                             22-APR-1999;
                                                                                                                           21-FEB-2001
                                                                                                                                                                                                                                                                     02-NOV-2000.
                                                                                                AAB37447;
                                          RESULT 15
                                                         AAB37447
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0; Gaps Query Match 85.3%; Score 586; DB 3; Length 122; Best Local Similarity 100.0%; Pred. No. 2.7e-59; Matches 110; Conservative 0; Mismatches 0; Indels Sequence 122 AA;

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Search completed: September 24, 2004, 14:08:38 Job time : 52.308 secs

us-10-661-784-3.rai

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RESULT 1
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Sequence 24
Patent No. 5
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1 GSGKDFVQPPTKICVGCPRD......VPWEKKIYPTVTVNHWECEF
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(/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-019-485-3
US-09-617-302-9
US-09-617-302-9
US-09-528-436B-2
US-09-715-932-14
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US-09-775-932-14
US-09-775-932-12
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US-09-617-302-8
US-09-617-302-10
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US-09-617-302-10
US-09-617-302-10
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Listing first 45 summaries
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Match
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Perfect score:
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Result No.

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MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IDN ES/2
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US, Application
FILING DATE: 9 February 1994
CLASSIFICATION NUMBER: US, Application
APPLICATION NUMBER: US, Application
APPLICATION NUMBER: Bertal No. 5472945 07/744,545
FILING DATE: 13 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A,
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-137 CII
TELEPHONE: (215) 568-589
TELERACION NOWERTION: NOWEMATION: TELEPHONE: (215) 568-589
TELEPHONE: AST029456
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH 117 amino acids
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81.2%; Score 559; DB 1; I
Best Local Similarity 100.0%; Pred. No. 2.3e-55;
Matches 105; Conservative 0; Mismatches 0;
US-09-019-485-4

US-09-314-77-3

US-09-314-77-3

US-09-314-77-3

US-09-241-376-3

US-09-228-436B-3

US-09-9617-302-6

US-09-97-6-594-37

US-09-976-594-37

US-08-649-303-17

PCT-US-95-07135-9

US-08-67-242-15

US-08-68-93-303-19

US-08-849-303-19

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9206809

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schmaier, Alvin H.
APPLICANT: Grang, Yongping
TITLE OF INVENTION: Mcdulation of Blood
TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
NUMBER OF SEGUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Commonwealth System of Higher Education
STREET: Building
CITY: Philadelphia
STREET: Building
CITY: Philadelphia
STREET: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.0%; Score 556.5; DB 5; Length 117; Best Local Similarity 93.8%; Pred. No. 3.3e-55; Matches 106; Conservative 1; Mismatches 1; Indels 5;
                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 XD
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOCTHWARE: WordPerfect 5.1
CURBENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06809
FILING DATE: 19910813
CLASSIFICATION 514
PRIOR APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 744,545
FILING DATE: 13 ANGUSE 1991
ATTORNEY/AGENT INFORMATION:
NATIORNEY/AGENT INFORMATION:
NATIORNEY/AGENT INFORMATION:
NATIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REPRENCE DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 117 amino acids
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Sequence 2, Application US/08832535 Patent No. 5919658

US-08-832-535-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SRVKPGFPKTIKTNDPGVLQAARYSVEKENNCTNDMFLFKESRITRALVQIVKGLKYMLE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 FVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 VEIGRITCKKNOHLRL-DDCDFQINHTLKQILSCYSEVWVVPW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MU
STATE: MU
ZIP: 20850
COMPUTER READABLE FORM:
MEDUTOR READABLE FORM:
MEDUTOR READABLE FORM:
MEDUTOR TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING-SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,485
FILING DATE:
CLASSIETCATION NUMBER: US/09/019,485
FILING DATE:
FLECOMUNICATION:
NAME: BENEON, ROBERT H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF265P1
TELEPHONE: 3013098504
TELEPHONE: 3013098439
INPORMATION FOR SEQ ID NO: 3:
ENGURNE CHRACTERISTICS:
LENGTH: 145 amino acids
STEPRANDENCS: SINGLE
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.8%; Score 163.5; DB 3 Best Local Similarity 31.6%; Pred. No. 9.4e-11; Matches 37; Conservative 22; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: U.i., Haodong
APPLICANT: V., Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: V. Guo-Liang
APPLICANT: V. Jian
TITLE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
                                                                       ATTORNEY DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Benson, Robert H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF265
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: DOPLOGY: linear
MOLECULE TYPE: protein
US-09-019-485-2
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09019485 Patent No. 6066617 GENERAL INFORMATION:
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TOPOLOGY: lin
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US-09-019-485-3
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QV 11 TRICORPED PROPERTY (13.5) Each 10.9 4-8-11; Adapta 13.5 (Deat Local Statistity 31.64) Precal No. 9.4-8-11; Marches 37; Conservative 22; Mismatches 45; Indels 13, Gape 3 a Savkroepertrikinberulanismustrykrinwizzakovyazkkrini (11.61) [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61] [11.61]
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CITY: Pa
STATE: C
COUNTRY:
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                                                                                                                                                                                                                     11 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 SRVKPGFPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 91
                                                                                                                                                                                                                                                                                   71 FVARETICSKESNEELTESCE---IKKLGOSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                                                                                                                                                                                                                                92 VEIGRITCKKRQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPW-----LQHFE 138
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                                                                                                                                             Gaps
                                                                                                                                             Indels 13;
                                                                                           Query Match 23.8%; Score 163.5; DB 3; Length 145; Best Local Similarity 31.6%; Pred. No. 9.4e-11; Matches 37; Conservative 22; Mismatches 45; Indels 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%; Score 163.5; DB 4
31.6%; Pred. No. 9.4e-11;
iive 22; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K,
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09528436B
Patent No. 6576745
GENERAL INRORMATION:
APPLICANT: Li, et al.
TITLE OF INVENTION: Human Cystatin F
FILE REFERENCE: PES65P1D1
CURRENT APPLICATION NUMBER: US/09/528,436B
CURRENT FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1999-04-03
PRIOR APPLICATION NUMBER: 08/832,535
PRIOR APPLICATION NUMBER: 08/832,535
PRIOR APPLICATION NUMBER: 60/014,795
PRIOR APPLICATION NUMBER: 60/014,795
RRICH RELING DATE: 1996-04-03
NUMBER: OF SEQ ID NOS: 16
SOUTHWARE: Patentin Version 3.2
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08791522
Patent No. 5935817
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Best Local Similarity 31.65
Matches 37; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-302-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-09-528-436B-2
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OPERATION SYSTEM. DOS

SOUTHWART THE COMPATION.

SOUTHWART APPLICATION DATA.

CURRENT APPLICATION NORTH.

PRIOR APPLICATION NORMEN.

TILINGO DATA.

ATTOMORY/GART NORMEN.

TILINGO DATA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 PTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYPI 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of British Columbia,
TITLE OF INVENTON: Production and use of Modified Cystatins,
FILE REFERENCE: 58069
FURENT APPLICATION NUMBER: US/09/75,932
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 1999-08-05
PRIOR PLILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08
PRIOR FILING DATE: 1998-08
PRIOR FILING DATE: 1998-08
SOFTWARE: OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 DEVARETICSKE----SNEELTESCETKKIGO--SLDCNAEVYVVPWE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 121;
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US-09-775-932-12
Sequence 12, Application US/09775932
Patent No. 6534477
GENERAL INFORMATION:
APPLICANT: University of British Columbia
TILLE OF INVENTION:
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT APPLICATION NUMBER: CA99/00717
PRIOR APPLICATION NUMBER: CA99/00717
                                                                                                                                                                                                                                                                                                         23.7%; Score 163; DB 3; Length 178; 34.0%; Pred. No. 1.4e-10; ive 20; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 FVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 VEIGRTTCKKNOHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPW 155
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20.2%; Score 138.5; DB 4
Best Local Similarity 31.5%; Pred. No. 4.9e-08;
Matches 34; Conservative 22; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-775-932-14
; Sequence 14, Application US/09775932
; Patent No. 6534477
; GENERAL INFORMATION:
; APPLICANT: University of British CA
TELECOMMUNICATION INFORMATION:
                                        TELEFAX: 415-845-4166
| INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISICS:
| LENGTH: 178 amino acids
| TYPE: amino acid
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| INMEDIATE SOURCE:
| CLONE: 30443
                         : 415-855-0555
415-845-4166
                                                                                                                                                                                                                                                                                                                                                           Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 35; Conserva
                         TELEPHONE:
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9 POERWYGELRDLSPDDPQVQKAAQAAVASYNMGSNSIYYFRDTHIIKAQSQLVAGIKYFL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TMEMGSTDCRKTRVTGDHVDLT-TCPLAAGAQQEKLRCDFEVLVVPWQ 115
                                                                                                                                                                                                                        Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                           70 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 149;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,030C
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                        Query Match 20.2%; Score 138.5; DB 4; Best Local Similarity 31.5%; Pred. No. 5.2e-08; Matches 34; Conservative 22; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.2%; Score 138.5; DB 2; Best Local Similarity 31.5%; Pred. No. 6.4e-08; Matches 34; Conservative 22; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Human Genome Sciences, Inc.
I: 9410 Key West Ave
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ni, Jian
APPLICANT: Vu, Guo-Liang
APPLICANT: Vu, Guo-Liang
APPLICANT: Rosen, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Cystatin E
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08461030C
Patent No. 5985601
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders, Erockes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF20.
TELEPHONE: 301-301-8504
TELEPHONE: 301-30-8439
PRIOR APPLICATION NUMBER: 60/6
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 12
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 149 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-461-030C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                   TYPE: PRT

ORGANISM: Homo sapiens
US-09-775-932-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Patent No. 6235708
Patent No. 6235708
Patent No. 6235708
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REPERENCE: 98-72
CURRENT FILING DATE: 1999-11-01
BARLIER APPLICATION NUMBER: 60/109,217
EARLIER FILING DATE: 1998-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                          90 TMEMGSIDCRKTRVTGDHVDLT-TCPLAAGAQQEKTRCDFEVLVVPWQ 136
70 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 111
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/744,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 20.2%; Score 138.5; DB 3; Best Local Similarity 31.5%; Pred. No. 6.4e-08; Matches 34; Conservative 22; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                              3: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                               Sequence 2, Application US/08744138
Patent No. 6011012
GENERAL INFORMATION:
APPLICANT: Gentz, Reiner L.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Human Cystatin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: BrOCKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PP20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301 309 8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 301 309 8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid

TOPOLOGY: linear

// MOLECULE TYPE: protein

US-08-744-138-2
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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## EARLIER APPLICATION NUMBER: 60/156,382
## EARLIER FLING DATE: 1999-09-28
## CANDARE: 1999-09-28
## CANDARE: PactSEQ for Windows Version 3.0
## CANDARE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen.Ltd.
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September 24, 2004, 14:05:18; Search time 36.576 Seconds (without alignments) 1095.549 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-661-784-3 687 1 GSGKDFVQPPTKICVGCPRD......VPWEKKIYPTVTVNHWECBF 127 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 Total number of hits satisfying chosen parameters:

1017041 seqs, 315518202 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_rodent:*
sp_virus:*
sp_virus:*
sp_vorlassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_organelle:*
sp_phage:*
sp_plant:* sp_archea:* sp_bacteria:* SPTREMBL Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q7yrp6 sus scrofa	P70517 rattus norv	Q63581 rattus norv	Q9qwl5 mus musculu	Q7z4j8 homo sapien	Q7zy91 xenopus lae	Q7syh2 xenopus lae	Q801e5 xenopus lae	Q9epx9 mus musculu	Q800s8 brachydanio	Q8cb17 mus musculu	Q801z5 cyprinus ca	Q9nh95 litomosoide	Q80y72 mus musculu	Q8k397 mus musculu	Q9d1b1 mus musculu
COTTAGENOO	ΩI	Q7YRP6	. P70517	. 063581	O9QWL5	Q7Z4J8	3 Q7ZY91	3 Q7SYH2	3 Q801E5	6X4EQ 1	8 080088	1 Q8CB17	3 Q801Z5	O9NH95	L Q80Y72	L Q8K397	1 Q9D1B1
	DB	9	11	11	17	4	13	13	13	11	13	11	13	'n	11	17	11
	% Query Match Length DB	140	423	430	167	167	462	462	465	140	455	388	464	148	140	146	149
	% Query Match	55.7	55.5	55.0	25.0	23.8	22.2	22.2	22.2	19.1	18.0	17.3	17.1	16.5	16.4	16.2	16.2
	Score	383	381	378	171.5	163.5	152.5	152.5	152.5	131.5	123.5	119	117.5	113.5	113	111	111
	Result No.	п	N	m	4	ß	9	7	80	6	10	11	12	13	14	15	16

	O22202 arabidopsis 022202 arabidopsis P93627 zea mays (m 039270 brassica ca 096401 mus musculu 0802n5 mus musculu 014502 cercopithec
Q98SR3 Q98SR3 Q98SR3 Q9801X6 Q901X65 Q904G9 Q904M8 Q904M8 Q904M8 Q904M8 Q91825 Q25620 Q41825 Q41825 Q41825 Q41836 Q41836 Q41836 Q68XXV6 Q9730 Q41836 Q9730 Q41836 Q9730 Q41836 Q9730 Q41836 Q9730 Q973	022202 P93627 Q41897 Q39270 Q9DAP1 Q80ZN5
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	W 4 4 4 4 4 W O H G W 4 R

ALIGNMENTS

SECUENCE FROM N.A.
Vonnahme K.A., Fernando S.C., Ross J.A., Ashworth M.D., DeSilva U.,
Vonnahme K.A., Fernando S.C., Ross J.A., Ashworth M.D., DeSilva U.,
Malayer J.S., Geisert R.D.;
"Porcine Endometrial and Conceptus Expression of Kininogens and Plasma
Kallikrein in Cyclic and Pregnant Gilts.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A321363; AAP85260.1; 24 NSPELBETLTHTITKLNAENNATEYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN 0; Gaps Sus scrofa (Pig). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus. Length 140; 55.7%; Score 383; DB 6; Length 14 78.9%; Pred. No. 2.8e-30; ive 5; Mismatches 15; Indels 140 140 140 140 141 15650 MW; 177837836603F777 CRC64; DI-CTT-2003 (TrEMBLrel. 25, Created) 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Low molecular weight kininogen (Fragment). 140 AA PRT; Query Match
Best Local Similarity 78.9
Matches 75; Conservative PRELIMINARY; NON TER NON TER SEQUENCE Q7YRP6 RESULT 1 Q7YRP6 g ઠે 8

84 BELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 118

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83 9

RESULT

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P70517

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K.P., Croyle M.L., Lingrel J.B.;
structure of a gene encoding rat T-kininogen.";
                           Gene 81.119-128 (1989).
EMBL; M29083; AAA42251.1; -
EMBL; M29083; AAA42251.1; JOINED.
EMBL; M29084; AAA42251.1; JOINED.
EMBL; M29085; AAA42251.1; JOINED.
EMBL; M29085; AAA42251.1; JOINED.
EMBL; M29087; AAA42251.1; JOINED.
EMBL; M29089; AAA42251.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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SEQUENCE 1
                  Primary
                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q9QWL5;
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Q9QWL5
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                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                    MEDLINE=83149311; PubMed=2579644;
Cole T., Inglis A., Nagashima M., Schreiber G.;
"Major acute-phase alpha(1)-protein in the rat: Structure, molecular cloning, and requiation of mRNA levels.",
Biochem. Biophys. Res. Commun. 126:719-724(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.5%; Score 381; DB 11; Length 423; 62.1%; Pred. No. 1.6e-29; ive 14; Mismatches 30; Indels (
                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Major acute phase a lppa-1 protein precursor (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                     Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F9E8BD3198547949 CRC64;
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Last sequence update)
Last annotation update)
                  423 AA.
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SEQUENCE FROM N.A.
MEDLINE=90034172; PubMed=2806908;
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423 AA; 46905 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
Rat T-kininogen (T-KG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 62.1%
les 72; Conservative
              PRELIMINARY;
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423
379
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          P70517
P70517;
01-PEB-1997 ('
01-PEB-1997 ('
01-OCT-2003 ('
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SEQUENCE
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SIGNAL
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Matches

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SEQUENCE FROM N.A.

STARAN-CSTSHIGGS, PubMed=11217651;

Kawai J., Shinnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Arakawa T., Hara M., Rohburner M., Bacukawa T., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Bacukawa T., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Bacalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Bacalov S., Cochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Bacalov S., Cochiwa H.,

Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Rohimi L., Salubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Radota K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Radota M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Radotone P., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,

Radota M., Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-F.,

Radota M., Rodriguez C., Whittaker C., Wilming L.,

Radota M., Rawaili H., Kohtsuki S.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                   252 GDDLFSLLPKNCRGCPREIPVDSPELKEALGHSIAQLNAQHNHIFYFKIDTVKKATSQVV 311
                                                                                                                                                                                                                                                                                                      3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                                63 AGKKYPIDFVARETTCSKESNBELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Sciurognathi, Muridae, Murinae, Mus.
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GO; GO:0004869; F:cysteine protease inhibitor activity; IEA. InterPro; IPR00010; Cystatin.
Pfam; PF00031; Cystatin; 3.
SWART; SW00043; CYSTATIN; 2.
PROSTE; PS00287; CYSTATIN; 2.
SEQUENCE 430 AA; 47618 MW; 45508DEF4BDC978C CRC64;
                                                                                                                                                                                         Length 430;
                                                                                                                                                                                         Match 55.0%; Score 378; DB 11; Length 4. Local Similarity 62.1%; Pred. No. 3.1e-29; les 72; Conservative 13; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morita M., Arakawa H., Yoshiuchi N.;
"A novel cystatin-like metastasis associated gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Murine CMAP (CYATIN F) (LEUKOCYSTATIN).
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us-10-661-784-3.rspt

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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 KDLI---SSVKPGFPKTIETNNPGVLKAARHSVEKFNNCTNDIFLFKESHVSKALVQVVK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 VEIGRITICKKNOHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPW------LQHFE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 FVARETICSKESNEELIESCE---IKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Similar to fetuin B.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;
NCBI_TAXID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cystatin F (Leukocystatin).

Memo sapienb (Human).

Eukarycia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Phelan M., Farmer A.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BT009825; AAP88827.1; -- SEQUENCE 167 AA; 18857 NW; E339025A5BD60177 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKKYFIDFVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.0%; Score 171.5; DB 11; Length 167; Best Local Similarity 35.5%; Pred. No. 3.4e-09; Matches 39; Conservative 22; Mismatches 42; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 167;
                                                                                                                     EMBL; AR015224, BA334940.1; -.
EMBL; AK004420; BAB33298.1; -.
HSSP; P01034; 1G96.
MGD; MG1:129821; Cst7.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IFR000010; Cystatin.
PR00011; cystatin; 1.
SMART; SM00043; CY; 1.
SEQUENCE 167 AA; 18847 MW; 61F776D8445095FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 163.5; DB 4; Length 31.6%; Pred. No. 2.1e-08; ive 22; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q724J8;
Q1-CGT-2003 (TrEMBLrel. 25, Created)
01-CGT-2003 (TrEMBLrel. 25, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7ZY91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q724J8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q72Y91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                              10 PIKICVGCPRDIPINSPELEETLIHI ----ITKLNAENNAIFYFKIDNVKKARVQVVAGK
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Cystatin domain fetuin-like protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African Clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JTM-2003 (TrEMBLrel. 24, Created)
01-JTM-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical histidine-rich protein (Fragment)
Xenopus laevis (African clawed frog). Fragment;
Membribia, Batzach, Chordata, Craniata, Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                5;
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                                                                                                                                                                                                                                                                                        DB 13; Length 462;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC043891, AAH43891.1;
InterPro; DR000010; Cystatin.
Pfam; PR00011; Cystatin.
Pfam; PR00013; Cystatin.
SMART; SM00043; CY; 2.
SEQUENCE 462 AA; 53185 MW; D7BAD339961739FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TSSTBS-wentral midgut,
Costa R.W.B., Mason J., Lee M., Amaya E., Zorn A.W.,
"Novel gene expression domains reveal early patterning of
                                                                                                                                                                                                                                                                                  Query Match
22.2%; Score 152.5; DB 13; Length
Best Local Similarity 38.8%; Pred. No. 8.4e-07;
Matches 33; Conservative 13; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 22.2%; Score 152.5; DB 13; Length Local Similarity 38.8%; Pred. No. 8.4e-07; les 33; Conservative 13; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endoderm.",
Submitred (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY260732; AAP82289.1; -
SEQUENCE 462 AA; 53186 MW; 796F92774CC27721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 SYFIQFTIKETDCMKTQENVVLSNC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 SYFIOFTIKETDCMKTQENVVLSNC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 KYFIDFVARETTCSKESNEELTESC 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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190 MPMGGGYFTQFAIMETNCTKKDAPQNPEACKALCGDQATYGFCKSSKVGSEEPEVECEIY 249
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STRAIR-CAPEL/GAJ TISSUE=Vagina;
STRAIR-CAPEL/GAJ TISSUE=Vagina;
MEDLINE=22354683; PubMed=1246681;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:553-573(2002).
MST. AKO37043; BAC29682.1; -.
MGD; MGI:1890221; Fetub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VVACKKYFIDFVARETICSKESNEELIES------CETKKLG-QSLDCNAEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQ-
                            90 RITCTK-SOINLID-CPFHDOPHLMRKALCSFQIYSVPWK----GTHSLINFSCK 138
                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
75 ETTCSKESNEELTESC---ETKKLGOSLDCNAEVYVVPWEKKIYPTVTVNHWECE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.0%; Score 123.5; DB 13; Length 455; 26.7%; Pred. No. 0.00063; Live 23; Mismatches 46; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Panio rerio fetuin-A.";

"Danio rerio fetuin-A.";

"Danio rerio fetuin-A.";

"Danio red (JAN-2003) to the EMBL/GenBank/DDBJ databases.

"EMBL; AX217758; AA061483.1;

"GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

"GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

"GO; GO:0007018; F:structural molecule activity; IEA.

"InterPro; IPR002453; Beta tubulin.

"InterPro; IPR00010; Cystatin.

"Fam; PF00031; Cystatin.

"Pfam; PF00031; Cystatin.

"PRNAT; SM0043; CX; 1.

"PRNAT; SM0043; CX; 1.

"PROSITE: PS00225; TUBULIN B AUTOREG; 1.

"EROSITE: AS00225; TUBULIN B AUTOREG; 1.
                                                                                                                                                                                                                 01-TUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Conservative
                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Liver;
                                                                                                                                                                                            080088;
01-JUN-2003 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fetuin beta.
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                                                                                                                                                                       080058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8CB17
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Q8CB17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PTKICVGCPRDIPTNSPELEETLTHT----ITKLNAENNATFYFKIDNVKKARVQVVAGK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C;
MEDLINE=21010502; PubWed=11144350;
Taupin P.J., Ray J., Fischer W.H., Suhr S.T., Hakansson K., Grubb A.,
Gage F.H.;
"FGF-2-Responsive neural stem cell proliferation requires CCg, a novel
autocrine/paracrine ccfactor.";
Neuron 28:385-397(2000).
EMBL; AF311741; AAG40283.1; -.
HSSP; P01034; 1G96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                             "Cell-autonomous and signal-dependent expression of liver and intestine marker genes in pluripotent precursor cells from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 465;
                                                                   MEDLINE-22480013; PubMed=12591597;
Chen Y., Jurgens K., Hollemann T., Claussen M., Ramadori G.,
Pieler T.;
                                                                                                                                                                                                         Wech. Dev., 120:277-288(2003).

EMBL, AY188284; AAO31610.1; -.
GO, GO:0004869; F:cystaine protease inhibitor activity; IEA.
IEAPPRO, IRRONOUGO, Cystatin.
Pfam; PF00031; cystatin; 2.
SMART; SM00043; CY; 2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0004869; F:cysteine protease inhibitor activity; IEA. InterPro; IPR00010; Cystatin. IEA. PR00031; cystatin; 1. SMARY; SM00043; CY; 1. PROSITE; PS00287; CY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.2%; Score 152.5; DB 13; Length 38.8%; Pred. No. 8.5e-07; iive 13; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                             NON TER 1 1
SEQUENCE 465 AA; 53528 MW; 0B403AB4F78BBFD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AA; 15517 MW; 3A563406DD58D785 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel, 16, Created)
01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYSTATIN C.
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Best Local Similarity 38.8%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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nes 32; Conserv
                                         SEQUENCE FROM N.A.
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NCBI_TaxID=8355
                                                                                                                                                                                              embryos.";
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Matches
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106

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Gaps

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SEQUENCE FROM
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                                                                                                                                                                                              73 ARETICSKESNEELTESC----ETKKLGQSLDCNAEVYVVPWEKKIYPTVTVNH-W--- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 CPDCPGLLPLHDPKGLESVKTALQKFNKESDHKSYFKLMEVGRISTÖWMFSGQSFFSQFA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 CVGCPRDIPINSPELEETLIHTITKLNAENNAIFYFKIDNVKKARVQ-VVAGKKYFIDFV 72
                                                                                                                                                                              14 CVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVA 73
                                                                                                                                                                                                                                                  74 RETICSKESNEELTESCEIKKLG--QSLDCNAEVYVVPWEKKIYPIVIVNHWECEF 127
                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 464;
                                                                                                                      17.3%; Score 119; DB 11; Length 388; 25.9%; Pred. No. 0.0015; ive 28; Mismatches 52; Indels
GO:0004869; F:cysteine protease inhibitor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.1%; Score 117.5; DB 13; Length
24.8%; Pred. No. 0.0025;
ive 23; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsal P.-L., Chang G.-D., Huang C.-J.; "Purification and cloning of carp fecuin."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AY225965; AAO74862.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800228; TUBULIN B AUTOREG; 1.
464 AA; 51698 MW; 7A54F71E44050895 CRC64;
                                                                                             388 AA; 42742 MW; 78CFAD73A8D8DC22 CRC64;
                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005874; C:microtubule; IEA.
GO; GO:0005874; C:microtubule; IEA.
GO; GO:0004869; F:cysteine protease inhibitor acti
GO; GO:0005198; F:structural molecule activity; II
GO; GO:0007018; P:microtubule-based movement; IEA.
InterPro; IPR002453; Beta tubulin.
InterPro; IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                   464 AA.
                                                                                                                                                                                                                                                                                                                                   PRT;
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GO; GO: 0004869; F. J. C. Statin.
InterPro; IRR0010; Cystatin.
InterPro; IRR01165; Fetuin.
                                                      SMART; SM00043; CY; 2.
PROSITE; PS01254; FETUIN 1; 1.
PROSITE; PS01255; FETUIN 2; 1.
                                        Pfam; PF00031; cystatin; 2. SMART; SM00043; CY; 2.
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                                                                                                          Query Match
Best Local Similarity 25...
Best Local 30, Conservative
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Best Local Similarity 24.8'
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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148 AA

PRT;

PRELIMINARY;

RESULT 13 Q9NH95 ID Q9NH95 AC Q9NH95;

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TISSUB-Testicle.

TESUB-Testicle.

TESUB-Testicle.

TESUB-Testicle.

Retransberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Retransberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ratusberg R.L., Feingold B.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Heishe F.,

RA Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

RA Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worden P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Raha S.S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S.W., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Ratesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Rodriguez A.C., Grimwood J., Smails G.M., Schme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 ELEETLIHTITKINAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETICSKESNEEL
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Pfaff A.W., Hoffmann W.H., Taylor D.W., Schulz-Key H.;

"Characterization and immunological properties of a cystein protease inhibitor of the filarial parasite Litomosoides sigmodontis.";

linhibitor of the filarial parasite Litomosoides sigmodontis.";
                                                                                                                                                  Chromadorea, Spirurida, Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF229113; AAF35896.1; -. GO; GO:0004869; F:cysteine protease inhibitor activity; IEA. InterPro; IFR000010; Cystatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 113.5; DB 5; 34.1%; Pred. No. 0.0017; iive 16; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 -TESCETKKLGQSLD--CNAEVYVVPWE
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Onchocercidae; Litomosoides.
NCBI_TaxID=42156;
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                                                                                                                           Litomosoides sigmodontis.
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Best Local Similarity
Matches 30; Conserv
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28 LEETLIHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESNEELT 87
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN -2003 (TrEMBLrel. 24, Last annotation update)
RIKEN cDNA 1110017811 gene (Fragment).
RIKEN cDNA 110017811 gene (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mu
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                                                                                                                                                                 EMBL, BC048646, AAH48646.1; -...
GO; GO: 0004699; F: cysteine protease inhibitor activity; IEA.
InterPro; IPR000010. Cystatin.
InterPro; IPR0001013; Cystatin.
Pfam; PF00011; Cystatin, 1.
Probom; PB0001231; Cystatin, C/M; 1.
SRART; SM00043; CY; 1.
SEQUENCE 140 AA; 16199 MW; 32633E99C4697DA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
16.4%; Score 113; DB 11; Length 140;
Best Local Similarity 29.4%; Pred. No. 0.0018;
Matches 25; Conservative 18; Mismatches 38; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027680; AAH77680.1; -.
GOO: GOO: GOO: FPRO00010; Cystatin.
Pfam; PP00031; Cystatin; 1.
SMART; SM00043; CY; 1.
                                                                                   Strausberg R.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 ASCPLOSSKLKKSLICKSLIYSVPW 126
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Matches 29; Conservative
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TISSUE=Mammary gland;
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Search completed: September 24, 2004, 14:10:18 Job time : 37.576 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 24, 2004, 14:04:32; Search time 8.636 Seconds (without alignments) 765.738 Million cell updates/sec Run on:

US-10-661-784-3 687 1 GSGKDFVQPPTKICVGCPRD......VPWBKKIYPTVTVNHWBCBF 127 Title: Perfect score: (Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES		ΩÏ	KNG HUMAN	KNL1 BOVIN	KNH1 BOVIN	KNL2 BOVIN	KNH2 BOVIN	KNG MOUSE	KNG RAT		KNT1_RAT	CYTF MOUSE	CYTF_HUMAN	CYTC_MACMU	CYTM HUMAN	CYTC_BOVIN	FETB_RAT	CYTC HUMAN	CYTC_SAISC	FETE HUMAN	CYTC RAT	CYTC MOUSE	CYT_BITAR	CYTT HUMAN	CYTC_RABIT			CYT_CHICK	CYTS RAT	CYIN HUMAN	CYTS HUMAN	CYT ONCKE	CYTX ONCVO		CYT_CYPCA
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P31727 sarcophaga Q9d269 mus musculu									
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122	165	345	66	137	142	135	352	367	
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ALIGNMENTS

RESU KNG	RESULT 1 KNG HUMAN ID KNG HUMAN STANDARD; PRT; 644 AA.
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	ykinin),
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RN	Tree Processing
ማ ር	SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
¥ ¥	582; Pub
RA	S.;
RT	"Cloning and sequence analysis of cDNAs for human high molecular
Y C	entillingelis. Framary screeceres
RL	UND INCHIANT PLEATIFFICACION (1985).
RN	[2]
RP	GENE STRUCTURE,
ž	ysyzy4; gubuchima D
¥ 6	יי ומעמפעד ויי יידי מכני
£ 2	"Structural organization of the human kininogen gene and a model for
RT	
RL	J. Biol. Chem. 260:8610-8617(1985).
RN	[3]
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XX	Mascall Chickens D Geosti
Z E	Jakasawa 1., Shiokawa m.,
X C	inase minister
10	nter recently are to the control of
R R	
RP	SECUENCE OF 379-644.
X	
RA	Lottspeich F., Kellermann J., Henschen A., Foertsch B.,
RA	Mueller-Esteri W.;
RT	lifetions and sequence or the light chain or
RT	Ž,
R. P. K.	Eur. J. Blochem. 152:30/-314(1985/. [6]
R P	SECUTENCE OF 381-389.
ž	MEDLINE=90255622; PubMed=4952632;
æ	
R	"Structural features of plasma kinins and kininogens.";
A K	red. Froc. 2/:52-5/(1906/. [6] 1
묘	DISULFIDE BONDS.
RA	Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
RT	"Disulfide bonds in bovine HWW kininogens.";

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                                          MEDLINE=22660472; PubMed=12754519;

MEDLINE=22660472; PubMed=12754519;

A Lhang H., Li X. "J. "Martin D.B., Ambersold R.;

A Lhang H., Li X. "J. "Martin D.B., Ambersold R.;

A Lang H., Li X. "J. "Martin D.B., Ambersold R.;

Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";

In Marzide chemistry, stable isotope labeling and mass spectrometry.";

In Markiningen plays an important role in blood coagulation by HWM-kininogen plays an important role in blood coagulation by helping to position optimally prekallkrein and factor XI next to factor XII; (3) HWM-kininogen inhibites the thrombin-and plasminiduced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HWM-kininogen shows a variety of physiological effects: (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and dluresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation of conceptors (4E) it is a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action); (5) LWM-kininogen is in contrast to HWM-kininogen not involved in blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P01042-2; Sequence=VSP_001261, VSP_001262;
-!- TISSUE SPECTRICITY: Plasma.
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
-!- SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
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GO:00007596; P:blood coagulation; NAS.
GO; GO:00310146; P:diuresis; NAS.
GO; GO:0006954; P:inflammatory response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P01042-1; Sequence=Displayed;
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Seikagaku 56:808-808(1984).
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PIR, A01280; KGHULI.
SWISS-2DPAGE; P01042; HGGNEW; HGNC. 1833; KNG.
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GO; GO:001047; P:natriuresis; NAS.
GO; GO:0006939; P:smooth muscle contraction; NAS.
InterPro; IPR00010; Cystatin.
InterPro; IPR000315; Kininogen.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
SMART; SMO0434; CX; 3.
PROSTIE; PS000287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; Alternative splicing; Pyrrolidone carboxylic acid.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                            (ASSOCIATED WITH CLOTTING ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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PPKAGAEPASEREVS (in isoform LMW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 618; DB 1; Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.0%; Score 618; DB 1; Length 64 Best Local Similarity 100.0%; Pred. No. 3.4e-51; Matches 116; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_001261.
Missing (in isoform LMW).
/FTId=VSP_001262.
/FTId=VSP_001262.
/FTId=VSP_01262.
/F1132B4CBAPBFBB7E_CRC64;
                                                                                                                                                                                                                                                              KININOGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH
                                                                                                                                                                                                                   KININOGEN.
KININOGEN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 AA
                                                                                                                                                                                                                                                      BRADYKININ.
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N-LINKED
O-LINKED.
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O-LINKED.
O-LINKED.
O-LINKED.
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O-LINKED.
O-LINKED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
KNL1 BOVIN STANDARD;
AC PO1046;
DT 21-JUL-1986 (Rel. 01, Created)
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2218
2267
340
370
169
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119
614
94
126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428
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3381
137
137
420
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us-10-661-784-3.rsp

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 262:2768-2779(1987).

FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)

LMM-kininogen inhibits the aggregation of thrombocytes; (3) the
active peptide kallidin that is released from LMM-kininogen shows
a variety of physiological effects: (3A) influence in smooth
muscle contraction, (3B) induction of hypotension, (3C)

SUBCELDULAR LOCATION: Extracellular.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=P01044-1; Sequence=External;
TISSUE SPECIFICTTY: Plasma.

FTM: Bradykinin is released from kininogen by plasma kallikrein.
MISCELLANBOUS: LMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting.
SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                             MEDLINE-83117859; PubMed-6572010;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
Primary Structures of bovine liver low molecular weight kininogen
precursors and their two mRNAs.",
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                                                                                                                                                                                                                                                                                                                                                         SECUENCE OF 19-378.
MEDIATR=87137530; PubMed=3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;,
Miyata T., Iwanaga S.;,
Miyata T., Iwanaga S.;,
Postine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
chain portion.
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kiningen, LMW I precursor (Thiol proteinase inhibitor) (Contains:
Bradykinin].
                                                                                                   Bos taurus (Bovine).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidea, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, V00426; CAA23709.1; ...
PIR; A01283; KGBOL1.
InterPro; IPR000010; Cystatin.
Emm, PR00031; Cystatin.
SWART; SW00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
PROSITE; PS00287; CYSTATIN; 2.
Thiol protease inhibitor; Bradykinin; Signal;
Pyrrolidone carboxylic acid.
SIGNAL 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OR 169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KININOGEN, LAW I.
HRAYY CHAIN.
BRADXKININ.
LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
PYROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=2;
Name=LMW 1;
IsoId=P01046-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=HMW I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
CHAIN
PEPTIDE
CHAIN
DOMAIN
DOMAIN
MOD RES
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=84014106; PubMed=6571699;
Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
"A single gene for bovine high molecular weight and low molecular weight kininogens.";
Nature 305:545-549(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 378-393.
MEDLINE=70180420; PubMed=4986212;
Kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323 (1970).
                                                                                                                                                                                                                                                                                                                                                                        4 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUS. 75170265; PubMed=1169237; Han Y.N., Komiya M., Iwanaga S., Suzuki T.; Han Y.N., Komiya M., Iwanaga S., Suzuki T.; Han Y.N., Komiya M., Iwanaga S., Suzuki T.; Studies on the primary structure of bovine high-molecular-weight kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein."; J. Blochem. 77:55-68(1975).
--- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDLINE=87137530; PubMed=3546295; Neto H., Hayashida H., Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.; Miyata T., Iwanaga S.; Miyata T., Iwanaga S.; Peris Miyata T., De amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kininogen, HWW I precursor (Thiol proteinase inhibitor) (Contains: Bradykinin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                    .;
0
N-LINKED (GLCNAC. . .) (PARTIAL)
N-LINKED (GLCNAC. . .)..
INTERCHAIN.
                                                                                                                                                                                                                                                                                             Length 436;
                                                                                                                                                                                                                               A -> T (IN REF. 1; CAA23709).; F01F7EB6814BCE6C CRC64;
                                                                                                                                                                                                                                                                                             64.0%; Score 440; DB 1; Length 43 70.4%; Pred. No. 1.8e-34; ive 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chain portion.";
J. Biol. Chem. 262:2768-2779(1987).
                                                                                                                                                                                                                                                        48427 MW;
                                                                                                                                                                                                                                                                                                                                         81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
        SEQUENCE OF 458-498
      Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNH1 BOVIN
P01044;
                                                                                                                                                                                                              DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                     DISULFID
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                                                  DISULFID
                                                                                                             DISULFID
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4

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HWW-kininogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HWW-kininogen inhibits the thrombin—and plasmininduced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HWW-kininogen shows a variety of physiological effects (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of other mediators of inflammation of nociceptors (4E3) release of other mediators of inflammation of nociceptors (4E3) release of inflammation (e.g. prostaglandins), (4F) it has a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWEL; V01491, CAA2735.1; -.

R EMEL; V01491, CAA2735.1; -.

R PIR; A01281; KGE0H1.

R InterPro; IPR00010; Cystatin.

R InterPro; IPR00319; Kininogen.

R PRINTS; PR0031; Cystatin; 3.

DR RNST; S00019; CY; 3.

DR PROSTIE; PS00281; CYSTATIN; 2.

Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

KW Thiol protease inhibitor; Bradykinin; Blood coagulation;

KM Thiol protease inhibitor; Bradykinin; Pyrrolidone carboxylic acid.

In 18 PROSTER:

PROSTER:

R HALL AND TOTAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P01046-1; Sequence=External;
TISSUE SPECIFICITY: Plasma.
PTM: Bradykinin is released from kininogen by plasma kallikrein.
SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSTAIN-LIKE 1.
CYSTAIN-LIKE 1.
CYSTAIN-LIKE 2.
CYSTAIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .) (OR 169).
N-LINKED (GLCNAC. .) (OR 169).
N-LINKED (GLCNAC. .) (PARTIAL).
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68890 MW; D16850BEFE3C55CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P01044-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRADYKININ.
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350
350
621 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=HMW I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=LMW
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CARBOHYD
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SEQUENCE
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CHAIN
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DOMAIN
DOMAIN
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253 KDFVQPPTRLCAGCPKPIPVDSPDLEEPLSHSIAKLNAEHDGAFYFKIDTVKKATVQVVA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain portion.";
J. Balol. Chem. 262:2768-2779(1987).

J. Balol. Chem. 262:2768-2779(1987).

LIMM-kininogen inhibits the aggregation of thrombocytes; (2)

LIMM-kininogen inhibits the aggregation of thrombocytes; (3) the active peptide Kallidin that is rateased from LNW-kininogen shows a variety of physiological effects: (3A) influence in smooth muscle contraction, (3B) induction of hypotension, (3C)

-1-SUBCELLULAR LOCATION: Extracellular.
                                                                                                  64 GKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                     313 GLXYSIVFIARETTCSKGSNEELTKSCEINIHGOILHCDANVYVVPWEEKVYPTV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ising—Information of the state 
                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kininogen, LMW II precursor (Thiol proteinase inhibitor) (Contains: Bradykinin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 19-376.
MEDLINE-87137530; PubMed=3546295;
MEDLINE-87137530; PubMed=3546295;
Miyata T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
"Bovine high molecular weight sand disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
Pyrimary structures of bovine liver low molecular weight kininogen
precursors and their two mRNRs. Proc. Natl. Acad. Sci. US.A. 80:90-94(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                       434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P01047-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=83117859; PubMed=6572010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000010; Cystatin.
Pfam; PF00031; Cystatin; 3.
SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTATIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; V00427; CAA23710.1; -. PIR; A01284; KGBOL2.
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01038; 1A90
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                                                                                                                                                                                                                                                                                                                                   BOVIN
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                                                                                                                                                                                                                                                                                                   KNL2_BOVIN
                                                                                                                                                                                                                                                                RESULT
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KDFVQPPTKI CVGCPRDI PTNSPELEETLTHTITKLNAENNATFYFKI DNVKKARVQVVA

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64.0%; Score 440; DB 1; Length 621; 70.4%; Pred. No. 2.7e-34; rive 14; Mismatches 20; Indels

81; Conservative

Similarity

Local

Best Loca Matches

Query Match

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Mon Sep

us-10-661-784-3.rsp

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MEDLINE=70180420; PubMed=4986212;
3 GKDFVQPPTKICVGCPRDIPTNSPELBETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S., "A single gene for bovine high molecular weight and low molecular weight kininogens.";
Nature 305:545-549(1983).
                                                                                                                                                                                                                                                                                    63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                             310 GGLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTV 365
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
8 FEB-2003 (Rel. 41, Last annotation update)
BradyKinin]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                    KININOGEN, LWW II.
HEAVY CHAIN.
BADYKININ.
LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 3.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N.LINKED (GLCNAC. .).
O-LINKED (GLCNAC. .).
N.LINKED (GLCNAC. .)
INTERCHAIN.
                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 19-376.
MEDI-INE-8713530; PubMed=3546295;
Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
Miyata T., Iwanaga S.;
                                                                                                                                                                                                                       Length 434;
                                                                                                                                                                                                                                      22; Indels
                                                                                                                                                                                                        48148 MW; 73A7079DE3E03430 CRC64;
                                                                                                                                                                                                                     Match 60.1%; Score 413; DB 1; Local Similarity 67.2%; Pred. No. 6.6e-32; les 78; Conservative 14; Mismatches 22.
protease inhibitor; Bradykinin; Signal;
                                                                                                                                                                                                                                                                                                                                           619 AA
                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=84014106; Pubmed=6571699;
        carboxylic acid.
                                                                                                                                                                                                                                                                                                                                           STANDARD;
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SEQUENCE OF 376-391
                                                                            portion.";
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          Pyrrolidone
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READ H. Nagases S. S. Shurth T.,

State H., Nagases S. S. Shurth T.,

Donds and of methionyl bonds in kininogen: cleavages of disulfide

B. J. Hologo and of methionyl bonds in kininogen: II.,

J. Hologomen. 67:313-331(1770).

R. J. Hologomen. 67:313-331(1770).

R. J. Hologomen. 67:313-331(1770).

R. MININOGO OF 37:455.

R. MININOGO OF 37:455.

R. MININOGO OF 37:455.

R. MININOGO OF 45:495.

R. J. Hologomen. 67:313-331(1770).

R. J. Hologomen. 77:3100-1252(1756).

R. SECURROCO OF 45:495.

R. MININOGO OF 45
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3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Nagido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Badiarelli R., Tomaru Y., Haeegawa Y., Nogami A., Sofonbach C., Gojobori T., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brack D., Brusic V., Chothia C., Corbani L.B., Cousins S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanal A., Kawaji H., Kawasawa Y., Kedcierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 AGKKYFIDFVARETICSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 GGLXYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
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STRAIN=CSPBL/6 X CBA; TISSTDE_Liver;
MEDILNE=97342556, PubMed=9199253.
Takano M., Kondo J., Yayama K., Otani M., Sano K., Okamoto H.;
"Molecular cloning of CDNAs for mouse low-molecular-weight and high-molecular-weight prekiningens."
Biochim. Biophys. Acta 1352:222-230(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
CYSTATIN-LIKE 3.
PYREOLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . ).
O-LINKED (GLCNAC. . . ) (OR 169)
N-LINKED (GLCNAC. . . ) (PARTIAN-LINKED (GLCNAC. . . )
N-LINKED (GLCNAC. . . )
N-LINKED (GLCNAC. . . ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                            398 T -> P.
401
454 H -> V.
68710 MW; F04320ABEBOEEDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 413; DB 1;
Pred. No. 9.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNG MOUSE STANDARD; PRT; 661 AA. 008677; 008676; Q91XK5; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-MCA-2004 (Rel. 43, Last annotation update) Kininogen precursor [Contains: Bradykinin].
                                                                                                                                                                       INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM LMW).
STRAIN=C57BL/6J; TISSUE=Placenta;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                    60.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 67.2% es 78; Conservative
                                                                                                                                                                                                                                                                                  264
                                                                                                                                                                                                                                                                                                                                                                                                  619 AA;
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   DOMAIN
MOD RES
CARBOHYD
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SEQUENCE
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CARBOHYD
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PRESCRIPTION OF THE NUMBER K. NOTION OF D. REMACCHARGES S. RENGRAPH M. STATISTICS C. Serple C. N. Sector N., Shinada K., Shadada K., Sandalin M., Schadder C., Semple C. N. Sector N., Shinada K., Sandalin M., Schadder C., Semple C. N. Sector N., Shinada K., Sandalin M., Schadder C., Semple C. N. Sector N., Shinada K., Sandalin M., Schadder C., Semple C. N. Sector N., Shinada K., Sandalin M., Schadder C., Semple C. N., Sector N., Shinada K., Sandalin M., Schadder C., Semple C. N., Sector N., Schadder K., Sendalin M., Schadder C., Semple C. N., Schadder K., Schadder C., Wang Y., Malander C., Semple C., Wang Y., Pallianum W., Saldanum N., Saldanum N.,
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NCBI_TaxID=10116;

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 VAGTKYVIEFIARETKCSKESNTELAEDCEIKHLGQSLDCNANVYMRPHENKVVPTV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                  pfam; PF00031; cystatin; 3.
PRINTS; PRO0334; KININGGEN.
SWART: SW00043; CY; 3.
PROSITE; PS00267; CYSTATIN; 1.
Glycoprotedi, Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Alternative Splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEYKGRLSKAGAEPAPERQAESSQVKQ (in jsoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 60.1%; Score 413; DB 1; Length 661; Local Similarity 66.7%; Pred. No. 1.1e-31; es 78; Conservative 11; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform LMW).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      774460258D58796E CRC64;
                                                                                                                                                                                                                                                            BRADYKININ.
KININOGEN LIGHT CHAIN.
                                                                                                                                                                                                                                    KININOGEN.
KININOGEN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                  CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P08954; P08933;
01-NOV-1988 (Rel. 09, Created)
10-NOV-1988 (Rel. 09, Last sequence update)
Kininogen precursor [Contains: Bradykinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 001263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 639 AA
                                                                                                                                                                                                                         POTENTIAL.
                                               EMBL, D84415; BAA19743.1; -. SMBL, D84415; BAA19742.1; -. EMBL, AKO05547; BAB24115.1; -. EMBL, BC18158; AAH18158.1; -. MGJ, MG1.1097105; KM9. MGJ, MG1.21097105; KM9. InterPro; IPR000010, Cystatin. InterPro; IPR002395; Kininogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73102 MW;
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RECURBLE OF 1-41 FROM N.A.

RECURBLE STQUENCE OF 1-41 FROM N.A.

RECURBLE ST137465; PubMed=3818599;

RECURBLE ST137469; PubMed=3818599;

RECURBLE ST137469; PubMed=381989;

RECURBLE ST137469;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fung W.-P., Schreiber G.;
"Structure and expression of the genes for major acute phase alpha 1-
procein (thiostatin) and kininogen in the rat.";
The Biol. Chem. 262:9298-9308(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCODE 10 Sequence=VSP_001265, VSP_001266;
-!- TISSUE SPECIFICITY: Plasma.
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
-!- PTM: Bradykinin is released from kininogens: the classical HWW/LWM kininogens and two additional LWW-like kininogens: T-I and T-II.
-!- SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                      Furnto-Kato S., Marsumoto A., Kitamura N., Nakanishi S., Purnto-Kato S., Marsumoto A., Kitamura the rat precursors for bradykinin and T-kinin, Structural relationship of kininogens with
                                                                                                 Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
"Differing expression patterns and evolution of the rat kininogen
                                                                                                                                                                                                                                                                                                                                             major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                      (ISOFORMS HMW AND LMW).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P08934-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 260:12054-12059(1985)
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SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                  Biol. Chem. 262:2190-2198(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Buffalo,
MEDLINE=87250580; PubMed=2439509;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM LMW).
MEDLINE=86008264; Pubmed=2413018;
                                                                             MEDLINE=87137443; PubMed=3029068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-65 FROM N.A.
                                                   SEQUENCE FROM N.A.
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56.5%;
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   NCBI_TaxID=10116;
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   R EMBL; Mlots. J. 1825486; A25486.
R PIR; A25486; A25486.
R PIR; A254865 A25486.
R InterPro; IPRO0010; Cystatin.
DR PRINTS; PRO031; Cystatin, 3.
DR PRINTS; PRO034; KININOGEN.
DR PRINTS; PRO034; CY; SMOO44; CYSTATIN; 2.
RW Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; KW Bradykinin; Blood coagulation; Inflammatory response; Signal; W Alternative splicing; Multigene family.
FY SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 GDDLFELLPEDCPGCPRNIPVDSPELKEALGHSIAQLNAENNHTFYPKIDTVKKATSQVV 312
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CEYKGRLLKAGAGPAPERQAEASTVTP (in isoform
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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006932;
01-8094-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-10988 (Rel. 43, Last annotation update)
T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiostatin) [Contains: T-kinin].
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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D3172DF94FF56AF5 CRC64;
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Missing (In isoform LMW)
/FTId=VSP_001266.
E -> K (IN REF. 2).
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EMBL, M11884; AAA41487.1; -.
EMBL; M14569; AAA41484.1; -.
EMBL; M14569; AAA41485.1; ALT_SEQ.
EMBL; M16455; AAA41482.1; -.
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639 AA;
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MEDLINE=87250580; PubMed=2439509;

Fung W.-F., Schreiber G.;

Fung W.-F., Schreiber G.;

Structure and expression of the genes for major acute phase alpha 1-
protein (thiostatin) and kininogen in the rat.";

J. Biol. Chem. 263:928-9308(1987).

-I- FUNCTION: Kininogens are plasma glycoproteins with a number of functions: (1) as precursor of the active peptide bradykinin they effect smooth muscle contraction, induction of hypotension and increase of vascular permeability. (2) They play a role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII. (3) They are inhibitor of thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 7-430 FROM N.A. MEDLINE=88127561, PubMed=2578992; MEDLINE=88127561, PubMed=2578992; MEDLINE=88127561, PubMed=2578992; Major acute phase alpha 1-protein of the rat is homologous to bovine kiningen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level."; FEBS Lett. 182:57-61(1985).
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                                                                                           ACKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVPWEKKIYPTV 118
                                                                  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: In response to an inflammatory stimulant. T-kininogen II synthesis is induced and the plasma concentration of T-kininogen I is raised. T-kininogen I is raised. PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, II IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S., Paruto-Kato S., Parimary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase
                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (Rel. 03, Created)
01-NOV-1996 (Rel. 09, Last sequence update)
115-NAR-2004 (Rel. 43, Last annotation update)
T-Kninogen I precursor (Major acute phase protein) (Alpha-1-NAP)
(Thiostatin) [Contains: T-kinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTION OF "5-430 FROM N.A., AND PARTIAL SEQUENCE. MEDIANE=86008266; PubMed=2413019; Anderson K.P., Heath E.C.; The relationship between rat major acute phase protein and the
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MISCELLANEOUS: Rats express four types of kininogens: the
      Best Local Similarity 62.1%; Fred. No. 1.6e-29;
Matches 72; Conservative 15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                             430 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chém. 260:12054-12059(1985)
                                                                                                                                                                                                                                                                                                             PRT;
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Mammalia, Eutheria, Rodentia;
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                                                                                                                                                                                                                                                                                                                                P01048; P04081;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        alternative splicing kininogens: T-I and
                                                                                                           SILLARITY: Contains 3 cystatin-like domains.
CAUTION: In addition to the conflicts described in the feature table, Ref.2 sequence differs from that shown in positions 257, 262, 268, 269, 295, 314, 315, 331, 332 and 389. In all those positions the alternate amino acid is the one present in T-II kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
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classical HMW and LMW kininogens produced by alternative s
of the same gene, and two additional LMW-like kininogens:
T-II.
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PIR; A23897; A23897.

PIR; A27115; A27115.

GlycosuiteDB; P01048; -.

InterPro; IPR000010; Cystatin.

PEam; PF0031; Cystatin; 3.

SMART; SMO0043; CY: A7.

PROSTIE: PS00287; CYSTATIN; 2.

Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family; Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
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LNC -> MDR (IN REF. 2).
V -> L (IN REF. 2).
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EMBL, M1661; AAA41570.1; -.
EMBL, M16454; AAA41568.1; -.
EMBL; X02299; CAA26162.1; ALT_SEQ.
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CHAIN
PEPTIDE
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MEDLINE-98293.57; PubMed=9632704;

MEDLINE-98293.57; PubMed=9632704;

A Halfon S., Ford U., Foster J., Dowling L., Lucian L., Sterling M.,

A Halfon S., Ford U., Foster J., Dowling L., Lucian L., Sterling M.,

A Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.,

A Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.,

T. Leukocystatin, a new class II cystatin expressed selectively by

RT hematopoietic cells.,;

J. Biol Chem. 273:16400-16408(1998).

C. - FUNCTION: Inhibits papain and cathepsin L but with affinities

C. - FUNCTION: Inhibits appain and cathepsin continue regulation

through inhibition of a unique target in the hematopoietic system.

CC - SUBCELLUAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                              62
                                                                                                                                                                         3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                             63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                   312 AGVIYVIEFIARETNCSKQSKTELTADCETKHLGQSLNCNANVYMRPWENKVVPTV 367
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cystatin F precursor (Leukocystatin) (Cystatin-like metastasis-associated protein) (CMAP).
                                                                                                                                            ö
                                                                                                        DB 1; Length 430;
                                                                                                                                         30; Indels
R -> G (IN REF. 2 AND 3).
A -> L (IN REF. 2).
DH -> ER (IN REF. 3).
P -> S (IN REF. 1).
W, FAEBB78FAF4723C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTIE; PROSTIE; CYSTATIN, FALSE NEG.
Thiol protease inhibitor; Glycoprotein; Signal.
SIGNL 1 18 POTENTIAL.
CYSTATIN 19 144 CYSTATIN F.
SITE 36 36 REACTIVE SITE.
SITE 80 84 SECONDARY AREA OF CONTACT.
DISULFID 123 143 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B5837334C1B4A89C CRC64;
                                                                                                        th 55.3%; Score 380; DB 1; Similarity 62.1%; Pred. No. 9e-29; 72; Conservative 14; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                      144 AA
                                                                         47715 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF031826; AAC40140.1; -. EMBL; AF031825; AAC40139.1; -.
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InterPro; IRRO0010; Cystatin.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 1.
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                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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   414
415
420
430
430 AA;
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36
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98 1
123 1
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089098;
CONFLICT
CONFLICT
CONFLICT
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                                                                                                        Query Match
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SEQUENCE FROM N.A.

MEDLINE=21638799; PubMed=11780052;

MEDLINE=21638799; PubMed=11780052;

MEDLINE=21638799; PubMed=11780052;

MEDLINE=21638799; PubMed=11780052;

MEDLINE=21638799; PubMed=11780052;

MEDLINE=21638799; PubMed=11780052;

MEDLINE=21638799; Medline M., Baare D.M., Beare D.M., Bearley U.B., Barley U.B., Barley W.B., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Chapman J.C., Clamp M., Clark G., Carter N.P., Coulson A., Coville G.J., Dhami P.D., Dunn M.R., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Garfham D.V., Gariffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., A. Huckle B., Huut A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., A. Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
                                                                                    63
                                                                                                                        83
                                                                                                         MEDLINE=99298157; PubMed=9632704; Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M., Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S., Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.; Lebecque S., Lebkocystetin, a new class II cystatin expressed selectively by hematopoletic cells.";
                                                                                  4 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98406133; PubMed=9733783;
Ni J., Fernandez M.A., Danielsson L., Chillakuru R.A., Zhang J.,
Gruba A., Su J., Gentz R., Abrahamson M.;
"Cystatin F is a glycosylated human low molecular weight cysteine
proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDILINE-20199571; PubMed=10945474;

Morita M., Hara Y., Tamai Y., Arakawa H., Nishimura S.;

"Genomic construct and mapping of the gene for CMAP

"Leukcoystatin/Cystatin F, CST7) and identification of a proximal novel gene, BSCv (C200rf3).";

Genomics 67:87-91(2000).
                                                                                                                                                                                                                                                                                                       CYTF HUMAN STANDARD; PRT; 145 AA.
076096; Q9UBD4;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cystatin F precursor (Leukocystatin) (Cystatin 7) (Cystatin-like metastasis-associated protein) (CMAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                                                                 64 GKKYFIDFVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPW 110
                                                                                                                                                                                         Length 144;
                                           42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morita M., Arakawa H., Yoshiuchi N.;
"Human homologue of murine CMAP.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
    DB 1,
  25.0%; Score 171.5; DB 1
35.5%; Pred. No. 1.7e-09;
iive 22; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 273:24797-24804(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 273:16400-16408(1998)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens (Human)
Query Match
Best Local Similarity
Matches 39; Conserv
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CYTF HUMAN
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Manuscialio W.H. Leverin M.P. 10796 L.J. WGLDY K., Wochtrey A.A.,

RAM THIS S.A., WHIRTY D., WOCCAWACHE L.J. WGLDY K., WORLTRY A.A.,

RAM THINGS S.A., WHIRTY D., WOCCAWACHE L.J. WGLDY K., WINGEROON T.,

RAM STRUCK K., SHENGER J., PRINCE M. PECK A.I.,

RAM C. C. SHENGER J., SERRE R., PRINCE T.A.V. PECK A.I.,

RAM C. C. SHENGER J., SHENGER S., SHENGER S.
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                                                                                                                             11 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
                                                                                                                                            32 SRVKPGFPKTIKTNDPGVLQAARXSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 91
                                                                                                                                                                                                                                                                                                                                                                                                                         71 FVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                                                                                                         92 VEIGRITCKROQHLRL-DDCDFQINHTLKQILSCYSEVWVVPW------LQHFE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                         13;
          BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

B2BCC4F76857CB0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 138.5; DB 1; Length 146; ilarity 27.9%; Pred. No. 2.4e-06; Conservative 25; Mismatches 52; Indels 11;
                                                                                   DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECONDARY AREA OF CONTACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F0B3BB774A29DF26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the cystatin family.
                                                                                23.8%; Score 163.5; DB 1
31.6%; Pred. No. 9.9e-09;
ive 22; Mismatches 45
                                                                                                                                                                                                                                                                                         15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: IPR000010; Cystatin.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 1.
 85 SE
110 BY
144 BY
62 N-
115 N-
16454 MW;
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HSSP; P01034; 1G96.
                                                                                 Query Match 23.8%
Best Local Similarity 31.6%
Matches 37; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                Cystatin C precursor.
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37 37
81 99 1
123 1
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99 1
124 1
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115 1
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Matches 34; Conserv
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ACT SITE
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SEQUENCE
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CARBOHYD
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CYTC_MACMU
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FIDFVARETICSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                  A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plokins R.F., Jordan H., Moore T., Mars J., Hsieh F.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzaten P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Pahey J., Helton E., Ketteman M., Madan A.W., Gay L.J., Hulyk S.W.,

Pahey J., Helton E., Ketteman M., Madan A.Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                            88
        67
    OPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKY
                              MEDLINE=21246880; PubMed=11348457;
Zeeuwen P.L., Van Vlijmen-Willems I.M., Jansen B.J., Sotiropoulou G.,
Cutfs J.H., Meis J.F., Janssen J.J., Van Ruissen F., Schalkwijk J.,
"Cystatin M/E expression is restricted to differentiated epidermal
keratinocytes and sweat glands: a new skin-specific proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97150844; PubMed=8995380; Sotiropoulou G., Anisowicz A., Sager R.; Identification, cloning, and characterization of cystatin M, a nc Cysteine proteinase inhibitor, down-regulated in breast cancer."; J. Biol. Chem. 272:903-910(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97256812; PubMed=9099741;
Mi J., Abrahamson M., Zhang M., Fernandez M.A., Grubb A., Su J.,
Yu G.L., Li Y., Parmelee D., Xing L., Coleman T.A., Gentz S.,
Thotakura R., Nguyen N., Hesselberg M., Gentz R.,
"Cystatin E is a novel human cysteine proteinase inhibitor with
structural resemblance to family 2 cystatins.";
J. Biol. Chem. 272:10853-10858(1997).
                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          149 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Prostate;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                  Cystatin M precursor (Cystatin E)
                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-MAR-2004 (Rel. 43, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                      (Human)
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143 CQ 144
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Ο
           J. Invest. Dermatol. 116:693-700(2001).

-!- FUNCTION: Shows moderate inhibition of cathepsin B but is not active against cathepsin C.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Restricted to the stratum granulosum of normal skin, the stratum granulosum/spinosum of psoriatic skin, and the secretory coils of eccrine sweat glands. Low expression levels are found in the nasal cartin.

-!- PIM: Substrate for transglutaminases. Acts as an acyl acceptor but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 PTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVOVVAGKKYFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 PQERWYGELRDLSPDDPQVQKAAQAAVASYNMGSNSIYYFRDTHIIKAQSQLVAGIKYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
inhibitor that is a target for cross-linking by transglutaminase.";
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 BY SIMILARITY.
146 BY SIMILARITY.
137 N-LINKED (GLCMAC. . ) (POTENTIAL)
16511 MM, 2076A78BFC9FACRC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 TMEMGSTDCRKTRVTGDHVDLT-TCPLAAGAQQEKLRCDFEVLVVPWQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 DFVARETICSKE----SNEELTESCETKKIGQ--SLDCNAEVYVVPWE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
12-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cystatin C precursor (Colostrum thiol proteinase inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A., SEQUENCE OF 66-83, AND CHARACTERIZATION
TISSUE=Cerebrospinal fluid, and Choroid plexus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM: 601891, -.
GO; GO:0004869; F:cysteine protease inhibitor activity;
GO; GO:000745; P:embryogenesis and morphogenesis; TAS.
InterPro; IPR000010; Cystatin.
                                                                                                                                                                                           -!- SIMILARITY: Belongs to the cystatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease inhibitor, Signal, Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 20.2%; Score 138.5; DB 1
1 Similarity 31.5%; Pred. No. 2.4e-06;
34; Conservative 22; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSTATIN M.
REACTIVE SITE.
SECONDARY AREA O
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U81233; AAB61305.1; -.
EMBL; BC031334; AAH31334.1; -.
HSSP; P01038; 1CEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00031; cystatin; 1.
SMART, SM00043; CY, 1.
PROSITE; PS00287; CYSTATIN; 1.
                                                                                                                                                                                                                                                                                                                                                                     EMBL; U62800; AAB06566.1; -. EMBL; U81233; AAB61305.1; -.
                                                                                                                                                                            not as an acyl donor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:2478; CST6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
149
36
113
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 601891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTC BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
CYTC_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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Matches
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350:589-597 (2000)

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CARBOHYD
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g
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                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 NEGGVQEALSFAVSEFNKRSNDAYGSRVVRVVRARKQVVSGANYFLDVELGRTTCTK--S 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 NSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETICSKESN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE=20407138; PubMed=10947975;
Olivier E., Soury E., Ruminy P., Husson A., Parmentier F., Daveau M.,
Salier J.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       CYSTATIN C. PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
                                                                                84 EELTESC-----ETKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWECE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 QANLDSCPFHNQPHLKREKL----CSFQVYVVPWMN----TINLVKFSCQ 147
                                                                                                                                                                                                                                                                                                                          Pfam; PF00031; cystatin; 1.
SMART, SM00043; CY; 1.
PROSITE; PS00287; CYSTATIN; 1.
Thiol protease inhibitor; Signal; Pyrrolidone carboxylic acid.
          Olsson S.-L., Ek B., Wilm M., Broberg S., Rask L., Bjoerk I., "Molecular cloning and N-terminal analysis of bovine cystatin identification of a full-length N-terminal region."; Biochim. Biophys. Acta 1343:203-210(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Fetuin-B, a second member of the fetuin family in mammals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             REACTIVE SITE.
SECONDARY AREA OF CONTACT
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EE740FE37CFB9F0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
20.0%; Score 137.5; DB
Best Local Similarity 28.8%; Pred. No. 3e-06;
Matches 32; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090X79;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fetuin-B precursor (IRL685).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 AA
                                                                                                                                                                                                                                                                                                                                                                             PROBABLE
                                                                                                                                                                                                                                                                                 EMBL; Y10811; CAA71771.1; -. HSSP; P01034; 1G96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
  MEDLINE=98094199; PubMed=9434110;
                                                                                                                                                                                                                                                                                                                 nterPro; IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA;
                                                                        SEQUENCE OF 37-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
SEQUENCE
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPW--EKKIYPTVT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 VVGPSYFVEYLIKESPCTQSQDSCSLQASDSEPVGL---CQGSLIKSPGVPPQRFKKTVT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VQPPTK-----ICVGCPRDIPTNSPELBETLTHTITKLNAENNATFYFKIDNVKKARVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FETUIN-B.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41532 MW; 066C0A5C3B03C878 CRC64;
- SUBCELLUIAR LOCATION: Secreted (Potential).
- TISSUB SPECIFICITY: Liver.
- SIMILARITY: Belongs to the fettin family.
- SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 135; DB 1;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.7%; Scor. 25.8%; Pred. No. ... 32, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 24, 2004, 14:09:13 Job time : 9.636 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00031; cystatin; 2.
SMART; SM00043; CY; 2.
PROSITE; PS01254; FETUIN 1; 1.
PROSITE; PS01255; FETUIN 2; 1.
                                                                                                                                                                                                                                                                                                                               EMBL; AJ242926; CAB62543.1; -. InterPro; IPR000010; Cystatin. InterPro; IPR001363; Fetuin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Repeat.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.89
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---CEF
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5.⊥.6	Compugen
 e version 5.1.6	- 2004
Gencore	(c) 1993
	Copyright

protein search, using sw model OM protein -

8; Search time 13.716 Seconds (without alignments) 890.662 Million cell updates/sec September 24, 2004, 14:06:08 Run on:

US-10-661-784-3 687 1 GSGKDFVQPPTKICVGCPRD......VPWEKKIYPTVTVNHWBCEF 127 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR 78: *
1: pirl: *
2: pir2: *
3: pir3: *

	Description	LMW	, HIMW	LMW.	HMM I	_	, HMW	딮	kininogen, HMW I p	major acute phase	T-kininogen, LMW I	major acute phase	gen	cystatin - bovine	υ	υ Ω	C - ra	ď	Ų	cystatin SA precur	cystatin precursor	cystatin S precurs		T-kininogen (clone	1	ŝ	cystatin S precurs	hypothetical prote	ecurs	onchocystatin - ne
SUMMERIES		! ! ! !																												
S O M	ID	KGHUL1	KGHUH1	KGBOL1	KGBOH1	KGBOL2	KGBOH2	A28055	A25486	A23897	B28055	KGRIM	KGRTT1	UDBO	CHCC	S07085	S10587	A28793	A36163	B29632	E005	JQ1470	S68034	868035	JC2040	UDHUP2	UDHUP1	T33740	491	A43428
	DB	-	н	-	н	 1	H	0	~	~	N	Н	Н	Н	н	N	0	N	7	~	H	~	Ŋ	N	٦	Н	٦	~	N	7
	Length	427	644	436	621	434	619	433	639	430	430	423	430	112	146	127	120	111	140	141	139	141	91	91	111	141	141	139	132	162
,	% Query Match	90.06	90.0	64.0	64.0	60.1	60.1	59.7	59.7	56.5	56.5	55.5	55.3	20.0	19.3	18.9	18.8	18.6	18.6	18.1	17.2	16.4	16.3	16.3	16.2	15.9	15.8	15.6	15.4	15.4
	Score	618	618	440	440	413	413	410	410	388	388	381	380	137.5	132.5	130	129	128	127.5	124.5	118.5	113	112	112	111	109.5	108.5	107		105.5
	Result No.		N	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50

sarcocystatin A pr	cystatin precursor	cystatin II - maiz	cystatin D precurs	hypothetical prote	alpha-2-HS-glycopr	cystatin-related e	cystatin - avocado	cysteine proteinas	fetuin precursor -	cysteine proteinas	Ω,	cystatin - maize	cystatin - field m	alpha-2-HS-glycopr	Ca2+ dependent lip
A43644	JC4536	JC4007	A47142	T33301	521094	A45361	JH0269	827239	A32827	T00752	S54828	JC4882	S65071	WOHU	TS0516
~	N	0	0	ď	0	0	N	α	0	N	~	N	N	н	7
122	133	135	142	143	345	139	100	135	375	125	134	134	199	367	592
8.4	14.8	14.2	14.1	13.9	13.8	13.6	13.4	13.3	13.3	12.9	12.9	12.9	12.8	12.8	12.3
H					ın	Ŋ	22	'n	ď	'n	s.	'n	80	88	'n
102	101.5	97.5	6	95.	94.5	93	92	91	91	88.5	88	88			84.5

ALIGNMENTS

kininogen, LMW precursor [validated] - human kininogen, LMW precursor [validated] - human N.Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N.Alternate names: appliens (man) c.Species: Homo sapiens (man) c.Species: Homo sapiens (man) c.Accession: A01280; B22276; A27900, A27699; A31905; A34030 C.Accession: A01280; B22276; A27900, A27699; A31905; A34030 R.Ochmistry 23, S691-S697, 1984 A.A. Sasaki, M. A.Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its idential A.Reference number: A90490; MUID:85122621; PMID:6441591

A; Molecule type: mRNA A; Residues: 1-427 < OHK>

A;Cross-references: GB:K02566; NID:g177889; PIDN:AAA35497.1; PID:g177890
R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J; Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low sheference number: A92544; MUID:85234582; PMID:2989293
A;Accession: B25276

A; Molecule type: mRNA A; Mesidues: 1-427 crAXA. A; Residues: 1-427 crAXA. A; Cross-references: GB:M11437; NID:g186751; PIDN:AAB59551.1; PID:g386853 A; Cross-references: GB:M11437; NID:g186751; PIDN:AAB59551.1; PID:g386853 R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Rauth, G.; Mueller-Esterl, W. B; Lottspeich, F.; Kellermann, J.; Henschen, A.; Rauth, G.; Mueller-Esterl, W. A; Title: Amino acid sequence of the light chain of human low molecular mass kininogen. A; Reference number: A27900

A; Accession: A27900

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A, Molecule type: protein A, Residues: 380-389 < KATl>
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A;Residues: 381-389 <KAT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A27899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A27699
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                                                                                                                                                                                                                                                                                                                            A;Accession: S32422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Accession: A91153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A24871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A31905
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                                                                                                                                                                                                                                                           Fed. Proc. 27, 52-57, 1968

A;Title: Structural features of plasma kinins and kininogens.

A;Title: Structural features of plasma kinins and kininogens.

A;Refeatence number: A91455; MUID:90225622; PMID:4952632

A;Contents: annotation; bradykinin groups precursor is produced from the same gene as the HWW form (s C;Comment: The LWW kininogen precursor is produced from the same gene as the HWW form (s C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; more position: 3427-3420; UMLM:24890
A; Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
C; Superfamily: Kininogen; cystatin homology
C; Superfamily: Kininogen; cystatin homology
C; Reywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyd
F;1-18/Domain: signal sequence #status predicted cSIG:
F;19-427/Product: LMW prokininogen (Kininogen I) #status predicted cMAT>
F;19-389;390-427/Product: LMW kininogen II #status predicted cMCH>
F;19-31/Domain: cystatin homology c(Y1).
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S. J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evoluti A;Reference number: A92545; MUID:85234583; PMID:2989294
A;Contents: annotation; gene organization
R;Pierce, J.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kilinogen, HMW precursor [validated] - human

N.Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen

N.Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen

N.Contains: bradykinin (kallidin I); HMW kininogen I; HWW kininogen II; low molecular we

(Species: Homo sapiens (man)

C; Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000

C; Accession: A01279; A22276; S32422; A91153; A24871; A27899; A27699; A31905; A34030; S02

R; Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.

Biochemistry 23, 5691-5697, 1984

A; Title: Isolation of a human cDNa for alpha-2-thiol proteinase inhibitor and its identi

A; Accession: A01279

A; Molecule type: mRNa

A; Molecule type: mRNa

A; Molecule type: mRNa

A; Molecule type: mRNa
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Fi264-375/Domain: Cystatin homology <CY2>
Fi264-375/Domain: Cystatin homology <CY3>
Fi380-389/Product: 1yx91-bradykinin (kallidin I) #status experimental <BDY>
Fi380-389/Product: Dradykinin (kallidin I) #status experimental <BDY>
Fi380-387/Product: LWW kininogen light chain #status experimental <LCH>
Fi380-427/Product: LWW kininogen light chain #status experimental <LCH>
Fi380-427/Product: LWW kininogen light chain #status experimental <LCH>
Fi380-427/Product: LWW kininogen light chain #status experimental chain #status predicted
Fi380-407,83-94.107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:
Fi380-350/Cleavage site: Met-Lys (kallikrein) #status experimental
Fi383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
Fi389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
Fi401/Binding site: carbohydrate (Thr) (covalent) #status absent
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R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low A;Reference number: A92544; WUID:85234582; PMID:2989293
A;Accession: A25276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 368
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Pred. No. 3.6e-50;
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Best Local Similarity 100.
Matches 116; Conservative
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A/Residues: 15.52, 1.5644 c.Thk.
A/Residues: 15.52, 1.5644 c.Thk.
A/Residues: 2.52, 1.5641 c.Thk.
A/Residues: 2.52, 1.5641 c.Thk.
A/Residues: 2.52, 2.541 c.Thk.
A/Residues: 2.52, 2.541 c.Thk.
A/Residues: 2.52, 2.541 c.Thk.
A/Residues: 2.52, 2.541 c.Thk.
A/Residues: 2.52, 2.521 c.Thk.
A/Residues: 2.52, 2.521 c.Thk.
A/Residues: 3.782, 2.782 c.Thk.
A/Residues: 3.782, 3.782 c.Thk.
A/Residues: 3.782 c.Thk.
A/
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A;Cross-references: GB:J00010; GB:V00426; NID:g163256; PIDN:AAA30604.1; PID:g163257
6;Cromment: The LWM kininogen precursor is produced from the same gene as the HWM form as C;Cromment: The LWM kininogen precursor is produced from the same gene as the HWM form as C;Cromment: Rininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Cromment: Bradykinin, released from kininogen by kallikrein, is.a potent vasodilator, is. xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splitcing; blood coagulation; cysteine proteinase inhibitor; glyor C;Keywords: alternative splitcing; blood coagulation; cysteine proteinase inhibitor; glyor F;1-15/Domain: signal sequence #status predicted <MGT>
F;19-15/Product: LWM kininogen I #status predicted <MAT>
F;19-15/Product: LWM kininogen I heavy chain #status predicted <HCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlterness: alpha-2-thiol proteinase inhibitor; preprokininogen
NyAlterness: alpha-2-thiol proteinase inhibitor; preprokininogen
NyOntains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A01283
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors and A;Reference number: A93984; MUID:83117859; PMID:6572010
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Fig. 130/Domain: cystatin homology <CY2>
Fig. 130-388/Product: bradykinin (kallidin I) #status predicted <BDY>
Fig. 130-388/Product: bradykinin (kallidin I) #status predicted <BDY>
Fig. 130-388/Product: LW kininogen I light chain #status experimental ALCH>
Fig. 140-46, 82-93, 106-125, 141-144, 205-217, 228-247, 263-266, 327-339, 350-369/Disulfide bonds: Fig. 17, 87, 168, 169, 197, 204/Binding site: carbohydrate (Asn) (covalent) #status predicted Fig. 189, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 190-20, 1
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A,Molecule type: mRNA
A,Residues: 1-436 <NAW>
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A; Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
A; Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
A; Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C; Superfamily: kininogen: cystatin homology captimental chitain signal sequence #status experimental chitain chitain signal sequence #status experimental chitain chitain signal sequence #status experimental chitain chitain cystatin homology correction #status experimental chitain cystatin homology correction #status experimental chitain cystatin homology correction cystatin cystatin homology correction cystatin homology correction cystatin homology correction cystatin homology correction cystatin homo
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144-253/Domain: cystatin homology < CV2>
144-253/Domain: cystatin homology < CV3>
1580-359/Pomain: dynamin homology < CV3
1580-359/Pomain: HW kininogen light chain #status experimental < CV3
159/Modified site: pyrcolidone carboxyric acid (Gln) (in mature form) #status experimental < CV3
159/Modified site: pyrcolidone carboxyric acid (Gln) (in mature form) #status experimental < CV3
159-359/Pomain: fire: carbohydrate (Asn) (covalent) #status experimental #status experimental #status experimental #status experimental #status experimental F;339/Modified site: Arg-Sez (Kallikrein) #status experimental #status #stat
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AyTitle: Structural features of plasma kinins and kininogens.

AyReference number: Agilysis WIUD:90255622; PMID:4952632

AyReference number: Animogen precursor and the LMW form are produced from the same gene cycomment: Kininogen precursor and the LMW form are produced from the same gene cycomment: Kininogen precursor and the LMW form are produced from the same gene cycomment: The HWW kininogen precursor and the Cycomment: The glycine/histidiae/lysine-rich region of HWW kininogen light chain is imported to the residue is present in the Kininogen prior to the release of bradykinin.

AyGene: GBB: KNG

AyCross-references: GBB:125256; OMIM:228960
Ajexperimental source: urine
Ajexperimental cupide the Pro-383 modified to 4-hydroxyproline
Ajexperimental contents
Ajexperimental systems
Ajexperimental
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A; Residues: 431-434 <STR>
A; Residues: 431-434 <STR>
A; Residues: 431-434 <STR>
A; Ritagama, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
B; Kitamuran, N.; Kitagama, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
A; Title: Structural organization of the human kininogen gene and a model for its evoluti
A; Reference number: A92545; MUD:8524583; PMID:2989294
A; Contents: annotation; gene organization
R; Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
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A;Residues: 450-452,'X',454,'X',456 <LIT>
R;Straczek, J:; Maachi, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabet, P.; Bellevil
FBBS Lett. 373, 207-211, 1995
A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like
A;Reference number: S68059; MUID:96033974; PMID:7589467
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F;577/Binding site: carbohydrate (Ser) (covalent) #status experimental
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Pred. No. 5.7e-50;
0; Mismatches 0;
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100.0%; Pre
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Best Local Simi
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Conservative

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GKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV
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A; Residues: 1-434 <NAW>
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A; Residues: 458-498 cHAN>
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga,
J. Biol. Chem. 262, 2768-2779, 1987
A; Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of C
A; Reference number: A92627; MUID:87137530; PMID:3546295
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 125-127,'I', 129-378 cSUE>
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 125-127,'I', 129-378 cSUE>
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1985
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1985
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1985
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1985
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1985
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1985
A; Residues: 'Z', 20-123,'I', 1985
A; Residues: 'Z', 20-123,'I', 1984
A; Residues: 'Z', 20-123,'I', 1984
A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 1984
A; Title: The amino acid sequence of the light chain of human high-molecular-mass kininog
A; Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
A; Sueyoshi, T.; Miyata, T.; Kato, H.; Lwanaga, S.
Seikagaku 56, 808, 1984
A; Title: Disulfide bonds in bovine HWW kininogens.
                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 378-393 «KAT.
A; Residues: 378-393 «KAT.
J; Molecules: 378-393 «KAT.
J; Biochem, 77, 55-68, 1975
A; Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami A; Reference number: A91938; MUID:75170265; PMID:1169237
                                                                                                                                                    and
                                                                                      Fixato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds
A;Reference number: A91923; MUID:70180420; PMID:4986212
                                                                      A; Cross-references: GB: V01491; GB: K01757; NID: 9491; PIDN: CAA24735.1; PID: 9492
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Pred. No. 2.4e-33;
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Best Local Similarity
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Gaps ö 63

KDFVQPPTKI CVGCPRDI PTNSPELEETLTHTI TKLNAENNATFYFKI DNVKKARVQVVA

14; Mismatches

81; Conservative

Matches

4 253

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C;Accession: A01284
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors and A;Reference number: A93984; MUID:83117859; PMID:6572010
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NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
NiAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text_change 22-Jun-1999
C; Accession: A01282; A91923; A91941; A91938; B2959
C; Accession: A01282; A91923; Firutto, S.; Tanada, T.; Nawa, H.; Nakanishi, S.
Nature 305, 545-549, 1983
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R;Kato, H.; Nagasawa, S.; Suzuki, T.
                                                                                                                                                                                       N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N'Contains: bradykinin (kalidin); Kininogen I; Kininogen II; prokininogen C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
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313 GLKYSIVFIARETICSKGSNEELIKSCEINIHGOILHCDANVYVVPWEEKVYPIV 367
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60.1%; Score 413; DB 1; I
Best Local Similarity 67.2%; Pred. No. 5.5e-31;
Matches 78; Conservative 14; Mismatches 22;
                                                                                                                                                                  kininogen, LMW II precursor - bovine
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62

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Firutto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikitegawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S. J. Biol. Chem. 262, 2190-2198, 1987
A; Title: Differing expression patterns and evolution of the rat kininogen gene family. A; Reference number: A92625; MUID:87137443; PMID:3029068
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                                  C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
                                                                                                                                                                                                                                                                                                                                     K-kininogen, LMW I precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
C.Accession: A28055
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A, Molecule type: mRNA

A, Note: the authors translated the codon CAA for residue 347 as Asn

C, Superfamily: kininogen; cystatin homology

C, Keywords: alternative spliding

C, Keywords: alternative spliding

F, 1-18/Domain: edgnal sequence #status predicted <MIC>

F, 19-639/Product: kininogen, HMW I #status predicted <MAT>

F, 19-233/Domain: cystatin homology <CX1>

F, 142-253/Domain: cystatin homology <CX2>

F, 264-375/Domain: cystatin homology <CX3>
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59.7%; Score 410; DB 2; Length 43
Best Local Similarity 66.4%; Pred. No. 1.1e-30;
Matches 77; Conservative 13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A28055
A;Molecule type: mRNA
A;Residues: 1-433 <FUR>
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <SIG>F;1-243/Product: K-khininogen, LMM I #status predicted <MAT>F;19-131/Domain: cystatin homology <CX1>F;14-253/Domain: cystatin homology <CX2>F;44-253/Domain: cystatin homology <CX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A92496; MUID:86008264; PMID:2413018
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N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Althorime, 67, 131-131, 1970

Althorime, 70, 131-131, 1970

Althorime, 197
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3 GKDEVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV

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Gaps

5

60.1%; Score 413; DB 1; Length 619; 67.2%; Pred. No. 8.2e-31; ive 14; Mismatches 22; Indels

Query Match Best Local Similarity 67.2³ Matches 78; Conservative

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62

63

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A;Residues: 'E',20-48;376-388,'R',390-419,'ER',422-430 <EN2>
C;Superfamily: kininogen; cystatin homology
C;Keylordas: glycoprotein; pyroglutamic acid
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-430/Pomain: cystatin homology <CY1>
F;19-430/Domain: cystatin homology <CY2>
F;141-252/Domain: cystatin homology <CY2>
F;19-130/Domain: cystatin homology <CY2>
F;19/Modified site: pyrrolidone acrboxylic acid (Gln) (in mature form) #status experiment
F;82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C)Accession: A01285
R;Cole, T.; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
FEBS Lett., 1825, 57-61, 1985
A;Title: Major acute phase alphal-protein of the rat is homologous to bovine kininogen ar A;Reference number: A01285; MUID:85127561; PMID:2578992
A;Accession: A01285
A;Accession: A01285
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C; Keywords: bradykinin; cystatin homology
C; Keywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflamm, fr. 11/Domain: signal sequence (fragment) #status predicted <SIG>
F; 12-423/Product: major acute phase alpha-1 protein #status predicted <MAT>
F; 12-423/Domain: cystatin homology <CY1>
F; 13-4245/Domain: cystatin homology <CX2>
F; 13-425/Domain: cystatin homology <CX2>
F; 13-425/Domain: cystatin homology <CX2>
F; 13-425/Domain: cystatin homology <CX2>
F; 12-123/Domain: cystatin homology <CX2>

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A;Residues: 1-423 <COL>
C;Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflammat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 GDDLFSLLPKKCFGCPKNIPVDSPELKEALGHSIAQLNAQHNHLFYFKIDTVKKATSQVV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-kininogen I precursor - rat
N'Alternate names: 73K protein; LMW kininogen T-I
N'Contains: bradykinin; T-kinin
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C,Accession: A01286; D25486; A28526; PL0193; JQ0027; B25488; A28525; S68036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major acute phase alpha-1 protein precursor - rat (fragment)
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b; Score 388; DB 2; Length 430;
b; Pred. No. 1.2e-28;
15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 423;
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Best Local Similarity 62.19
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Major acute phase alpha-1 protein (version 2) - rat
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiDate: 19-May-1898 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C;Accession: A23897; B23897
B;Anderson, K.P:; Heath, B.C.
J. Biol. Chem. 260, 12065-12011, 1985
A;Itle: The relationship between rat major acute phase protein and the kininogens.
A;Reference number: A23897; MUID:86008266; PMID:2413019
A;Molecule type: protein
A;Residues: D-14 <AMD1>
A;Residues: D-14 <AMD1>
A;Residues: S-430 <AMD2>
A;Molecule type: mRNA
A;Residues: S-430 <AMD2>
A;Molecule type: mRNA
A;Residues: GB:M11661; NID:9205307; PIDN:AAA11570.1; PID:9205308
A;Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 415
C;Superfamily: kininogen; cystatin homology <CX1>
F;141-252/Domain: cystatin homology <CX1>
F;263-374/Domain: cystatin homology <CX3>
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A; Residues: 1-430 «FURA
A; Residues: 1-430 «FURA
A; Residues: 1-430 «FURA
B; Ritagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. (Them. 262, 2130-2198, 1987
A; Title: Differing expression patterns and evolution of the rat kininogen gene family.
A; Reference number: A92625; MUD:87137443; PMID:3029068
A; Rocession: E25466
A; Molecule type: DNA
A; Reto, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
Biol. (Chem. 263, 973-979, 1988
A; Title: Purification and characterization of rat T-kininogens isolated from plasma of A; Reference number: A92729; MUD:88087226; PMID:3121623
A; Residues: 'E', 20-25; 'MD', 28-48, 376-430 «ENJ>
A; Recession: C28526
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Co-Unn-1998 #sequence revision 20-Jun-1989 #text_change 12-Dec-1997
C;Accession: B28055; E25486; B28526; C28526
C;Accession: B28055; E25486; B28526, X; Kitamura, N.; Nakanishi, S.
T;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
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253 GDDLFELLPEDCPGCPRNIPVDSPELKEALGHSIAQİLNAENNHTFYFKIDTVKKATSQVV 312
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thes 29; Indels
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A;Reference number: A92496; MUID:86008264; PMID:2413018
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; Score 388; DB ; Pred. No. 1.2e-15; Mismatches

56.5%;

Query Match
Best Local Similarity 62...
Best To 72; Conservative

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A; Accession: B28055

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R;Hirado, M.; Tsunasawa, S.; Sakiyama, F.; Niinobe, M.; Fujii, S.
FEBS Lett. 186, 41-45, 1985.
A;Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase in
A;Reference number: A01271; MUID:85231205; PMID:3891407
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A. Reference number: S10216; MUID:90303202; PMID:2363674
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                                 F.141-252/Domain: cystatin homology <CY2>
F.263-374/Domain: cystatin homology <CY2>
F.263-374/Domain: cystatin homology <CY3>
F.378-386/Product: bradykinin #status predicted <BDX>
F.19/Modified site: pyrrolidone carboxylic (Gln) (in mature form) #status experiment F.19/Modified site: pyrrolidone carboxylic carboxylic (Gln) (covalent) #status predicted F.82.126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted F.83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status
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C'Species: Bos primigenius taurus (cattle)
C'Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 06-Dec-1996
C'Accession: A01271
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A,Cross-references: EMBL:X52255; NID:g30257; PIDN:CAA36497.1; PID:g296643
A,Cross-references: EMBL:X52255; NID:g30257; PIDN:CAA36497.1; PID:g296643
R;Abrahamson, M.; Grubb, A.; Olafsson, I.; Lundwall, A.
FEBS Lett. 216, 259-233, 1987
A;Title: Molecular cloning and sequence analysis of cDNA coding for the px
A,Reference number: S00004; MUID:87219149; PMID:3495457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 EELTESC-----ETKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWECE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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A.Residues: 1-112 <HIR>
C.Superfamily: cystatin; cystatin homology
C.Keywords: colostrum; cysteine proteinase inhibitor
F;2-112/Domain: cystatin homology <CYS>
F;48-52/Region: inhibitory #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.0%; Score 137.5; DB 1
llarity 28.8%; Pred. No. 7.5e-06;
Conservative 25; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                             55.3%; Score 380; DB 1; 62.1%; Pred. No. 6.7e-28; ive 14; Mismatches 30;
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                  F,19-130/Domain: cystatin homology <CYl>
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Best Local Similarity 62.1%;
Matches 72; Conservative 1
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es 32; Conserv
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A; Medicus: 330-420, T, 422-429, T, 421-429, T, 421-429
R; Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A; Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and nhibitor.
A; Reference number: A92496; MUID:86008264; PMID:2413018
A; Accession: A01286
A; Accession: A01286
A; Residues: 1-430 < PUR>
A; Ritagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A; Ritle: Differing expression patterns and evolution of the rat kininogen gene family. A; Reference number: A92625; MUID:87137443; PMID:3029068
A; Residues: 37-430 < PUR
A; Reference number: A92729; MUID:88087226; PMID:3121623
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C;Superfamily: kininogen; cystatin homology
C;Superfamily: kininogen; cystatin homology
C;Cywywords: acute phase; bradykinin; cystatine proteinase inhibitor; duplication; glycopz
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-430/Product: T-kininogen I #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Modecule type: protein
A; Residues: 'E',20-48;376-430 <ENJ>
R; Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A; Title: identification of a protein increasing in serum of Nagase analbuminemic rats be
A; Reference number: PL0193; MUID:90216390; PMID:2108948
                                                                                                                 precursors for bradykinin and
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Afracial type: clone pSG17
CCOmment: At least three types of LMM kininogen precursors are present in rat plasma, ceding bradykinin.
CCOmment: Trkininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after CCOmment: Trkininogens are produced in response to an inflammatory stimulant:
CCOmment: The T-kininogens are produced in response to an inflammatory stimulant:
CCOMMENT: The T-kininogens are produced in response to an inflammatory stimulant:
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A;Molecule type: protein
A;Residues: 27-53 <POP>
A;Residue also corres: urine, kidney disease
A;Note: truncated fourse with amino ends at positions 35 and 36 of the precursor were also R;Grubb, A.; Lofberg, H.; Barrett, A.J.
FEBS Lett. 170, 370-374, 1984
A;Title: The disulphide bridges of human cystatin.
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27.0%;
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Best Local S:
Matches 33,
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S07085
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A; Mesidues: 1-24, Tr, 26-146 <SAI>
A; Cross-references: GB:M27889; GB:M27890; GB:M27891; NID:g181385; PIDN:AAA52164.1; PID:g
R; Ghiso, J.; Cowan, N.; Frangione, B.
Biol. Chem. Hoppe-Seyler 389, 205-208, 1988
Biol. Chem. Hoppe-Seyler 389, 205-208, 1988
A; Title: Isolation of a sequence encoding human cystatin C. Conservation of exon-intron
A; Reference number: S02751; MUID:89076507; PMID:3264504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-146 <LEV>
A,Cross-references: CB:X61681, NID:g30367, PIDN:CAA43856.2, PID:g4490944
A,Note: the cystatin C gene isolated from the brain of an Icelandic patient with heredit
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A;Residues: 37-93,'Q',95-146 <GHI>
A;Residues: 37-93,'Q',95-146 <GHI>
A;Residues: 37-93,'Q',95-146 <GHI>
A;Riruk, W.; Brzin, J.; Longer, M.; Ritonja, A.; Eropkin, M.; Borchart, U.; Machleidt, W.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1487-1496, 1983
A;Title: Protein inhibitors of cysteine proteinases. III. Amino-acid sequence of cystati
A;Reference number: S01461; MUID:84110059; PMID:6662498
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A;Title: The human cystatin C gene (CST3) is a member of the cystatin gene family which A;Reference number: A33400, MUID:89350949; PMID:2764935
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R;Levy, E.; Lopez-Otin, C.; Ghiso, J.; Geltner, D.; Frangione, B.
J. Exp. Med. 159; 1771-1778, 1989
A;Title: Stroke in Icelandic patients with hereditary amyloid angiopathy is related to A;Reference number: JL0095; MUID:89235594; PMID:2541223
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A; Residues: 27-49, XXX', 52-64 COLA>
A; Residues: 27-49, XXX', 52-64 COLA>
A; Residues: 27-49, XXX', 52-64 COLA>
A; Robers: 27-49, XXX', 52-64 COLA>
A; Robers: 27-64 Colaboration and the second and the second and se
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A,Residues: 27-76 <BRZ>
R;Olafsson, I.; Gudmundsson, G.; Abrahamson, M.; Jensson, O.; Grubb, A.
Scand. J. Clin. Lab. Invest. 50, 85-93, 1990
A;Title: The amino terminal portion of cerebrospinal fluid cystatin C in hereditary
A;Reference number: A60552; MUID:90193615; PMID:2315647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Brzin, J.; Popovic, T.; Turk, V.
cochem. Biophys. Res. Commun. 118, 103-109, 1984
Title: Human cystatin, a new protein inhibitor of cysteine proteinases.
Reference number: A32732; MUID:84128015; PMID:6365094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 82-119 <6H2>
A;Cross-references: EMBL:W27769
A;Note: the authors translated the codon ACC for residue 105 as Thr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 27-73 <TUR>
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                                                           lecule type: mRNA
sidues: 1-146 <AB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JL0095
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S00004
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A;Molecule type: protein
A;Residues: 27-49;106-146 <BER>
C;Comment: This protein is found in the post-gamma-globulin fraction of cerebrospinal flu
f patients whith certain autoimmune diseases.
C;Comment: This protein is an inhibitor of cysteine proteinases and may serve an importar
C;Comment: A mutant cystatin C, with 94-Gln, is deposited in hereditary cerebral hermorrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cystatin C precursor - rat (fragment)
Cystatin C precursor - rat (fragment)
Cystatin C precursor - rat (fragment)
Cystatin C precursor - rat (Norway rat)
Cybate: 0.1 Dec-1993 #sequence_revision 03-Aug-1995 #text_change 16-Jul-1999
Cybate: 0.0 Dec-1993 #sequence_revision 03-Aug-1995 #text_change 16-Jul-1999
Cybate: 0.0 Dec-1993 #sequence_revision 03-Aug-1995 #text_change 16-Jul-1999
RyCole, T.; Dickson, P.W.; Esnard, F.; Averill, S.; Risbridger, G.P.; Gauthier, F.; Schrefilder, T.; Dickson, P.W.; Esnard, F.; Averill, S.; Risbridger, G.P.; Gauthier, F.; Schrefilder on number: 807085
A;Reference number: 807085
A;Retus: preliminary
A;Residues; 1-127 *COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 81/3; 119/3
Cstoperfamily: oystetin; oystetin homology
C;toywords: amyloid; oysteine proteinase inhibitor; extracellular protein; hydroxyproline
F;1-26/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                               susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 FIDFVARETICSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 KPPR--LVGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 QPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKY
                                                                                                                                                                   to proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;35-146/Domain: cystatin homology <CYS>
F;81.87/Region: inhibitory #status predicted
F;29/Modified site: hydroxyproline (Pro) (partial) #status experimental
F;99-109,123-143/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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A;Reference number: S01462
A;Contents: annotation; disulfide bonds
R;Berti, P.J.; Storer, A.C.
Bochem. J. 302, 411-416, 1994
A;Title: Local pH-dependent conformational changes leading
A;Reference number: S55305; WUID:94379969; PMID:8092991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-146/Product: cystatin C #status experimental <MAT>
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A;Reference number: S01337; MUD:88313020; PMID:3044831
A;Accession: S01337
A;Molecule type: protein
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Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
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A;Residues: 8-49 cESN>
R;Esnard, A.; Esnard, F.; Guillou, F.; Gauthier, F.
Rissnard, A.; Esnard, F.; 1992
A;Title: Production of the cysteine proteinase inhibitor cystatin C by rat Sertoli cells
A;Reference number: S21109
A;Reference number: S21109
A;Reference number: S21109
A;Redicule type: protein
A;Residues: 8, 'XX',11-20 < cS2>
C;Superfamily: cystatin cystatin homology
C;Keyworfs cystatin homology < cystatin homology < cYS>
F;80-90,104-124/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 OPPTKICVGCPRDIPTNSPELESTLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.9%; Score 130; DB 2; Length 127;
Best Local Similarity 28.0%; Pred. No. 4.3e-05;
Matches 30; Conservative 28; Mismatches 43; Indels
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September 24, 2004, 14:08:41; Search time 44.704 Seconds (without alignments) 913.519 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                  OM protein - protein search, using sw model
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US-10-661-784-3 687 1 GSGKDFVQPPTKICVGCPRD......VPWEKKIYPTVTVNHWECEF 127 Perfect score: Sequence: Title:

1349238 segs, 321558718 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched: 1349238 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep: %
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: %
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: % /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 82, Appl	Seguence 70, Appl	Sequence 29, Appl	Sequence 72, Appl	Sequence 74, Appl	Sequence 84, Appl		Sequence 215, App	Sequence 2, Appli	Sequence 197, App	Sequence 1, Appli	Sequence 14, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 16, Appl
	QI	US-10-162-335-82	US-10-162-335-70	US-09-919-039-29	US-10-162-335-72	US-10-162-335-74	US-10-162-335-84	US-10-316-253-217	US-10-316-253-215	US-10-329-428-2	US-09-746-783-197	US-09-969-834-1	US-09-775-932-14	US-09-775-932-12	US-09-940-497-2	US-08-849-303-16
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	Watch Length DB	390	398	427	615	644	644	424	430	145	167	178	121	128	149	112
o}e }	Match	90.06	90.0	90.0	90.0	90.0	90.0	55.5	55.3	23.8	23.8	23.7	20.2	20.2	20.5	20.0
	Score	618	618	618	618	618	618	381	380	163.5	163.5	163	138.5	138.5	138.5	137.5
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Sequence 16, Appl Sequence 24, Appl	Sequence 2, Appli	e 12	17	'n	'n	m	4	-	equence 1	4	n	Φ	ω	Φ	-	ω	σ	ө 4	13	Н	4	₹#	26	9	18, 4	- 138 - 138	ednence 8,	Sequence 24, Appl
6 US-10-655-136-16 US-09-775-932-24	US-09-775-9	0-695	845	-940-	US-09-969-834-3	ď	-976 - 0	US-10-655-	0-695-1	US-10-	US-10-257-3	US-10-210-1	US-10-210-1	.2 US-10-210-172-84	US-10-210-172	.2 US-10-210-172-80	US-10-315	.2 US-09-978-360A-425	3 US-08-849-303-19	-629-	US-10-376-	14 US-10-376-564-48	3 US-08-849-303-26	0-655-13	08-849-303-1	6 US-10-655-136	-09-775-932-	3 US-08-849-303-24
112 1	120 9	120 1	~	146 9	146 9	146 1	146 1	146 1	146 1	249 1	641 1	317 1	345 1	356 1	369 1	369 1	382 1	382 1	127 8	127 1	140 1	140 1	111	111	140 8	•		141
5.5	132.5 19.3	.5	.5	5.	.5	.5	2.5 1	132.5 19.3	2.5 1	2.5	2.5 1	131.5 19.1	131.5 19.1	1.5 1	131.5 19.1	1.5 1	1.5	1.5	0	-	.5	.5	28 1	28 1	.5 18.	.5	124.5 18.1	124.5 18.1
16	8	19	20	21	22	23	24		26		28		30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	4 .

ALIGNMENTS

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APPLICANT: Parturajan, Merana
APPLICANT: Pera, Carol B. A.
APPLICANT: Reastelli, Luca
APPLICANT: Shimkets, Richard A.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Sethusen, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zethusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/162,335
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR PRIOR PLING DATE: 2001-06-04
Sequence 82, Application US/10162335 Publication No. US20040009480A1 GENERAL INFORMATION:
                                                                         APPLICANT: Anderson, David W.
APPLICANT: Baungartner, Jason C.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Gangal, Stacie J.
APPLICANT: Gangali, Esha A.
APPLICANT: Gangali, Esha A.
APPLICANT: Gangali, Esha A.
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Hyalt, Tord
APPLICANT: Hyalt, Tord
APPLICANT: Hyalt, Tord
APPLICANT: Kekuda, Ramesh
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                                                                                                                                                                                                                                                                                                                                                                                 Li, Li
MacDougall, John R.
Malyankar, Uriel M.
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Sequence 29, Application US/09919039
| Sequence 29, Application US/09919039
| Publication No. US20030108871A1
| GENERAL INFORMATION AND US20030108871A1
| APPLICANT KASSET, MATTHEW R. TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
| FILE REPERENCE: PA-0033 US/09/919,039
| CURRENT APPLICATION NUMBER: US/09/919,039
| CURRENT PILING DATE: 2000-09-09
| PRIOR PAPPLICATION NUMBER: 60/222,113
| PRIOR PAPPLICATION NUMBER: 60/222,113
| PRIOR PILING DATE: 2000-07-28
| NUMBER OF SEQ ID NOS: 401
| SEQ ID NO 29
| LENGTH: 427
| TYPE: RT
| ORCANISM: Homo sapiens
| FRATURE: FRA
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                                                                         PRICR APPLICATION NUMBER: 60/296,404
PRICR APPLICATION NUMBER: 60/296,404
PRICR FILING DATE: 2001-06-06
PRICR FILING DATE: 2001-06-06
PRICR PELING DATE: 2001-06-06
PRICR FILING DATE: 2001-06-01
PRICR FILING DATE: 2001-06-12
PRICR FILING DATE: 2001-06-12
PRICR FILING DATE: 2001-06-12
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PRICR PLICATION NUMBER: 60/299,285
PRICR FILING DATE: 2001-06-14
PRICR FILING DATE: 2001-06-15
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; OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1
US-09-919-039-29
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90.0%; Score 618; DB 15;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 116; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-70
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APPLICANT: Parturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method CHEREN APPLICANT: 2001-2171 B. 
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PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR PLING DATE: 2010-06-06
PRIOR PLING DATE: 2010-06-11
PRIOR PLING DATE: 2001-06-11
PRIOR PLING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR PLING DATE: 2001-06-14
PRIOR PLING DATE: 2001-06-14
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PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-26
PRIOR PRIOR APPLICATION NUMBER: 60/300,883
PRIOR PLING DATE: 2001-06-26
PRIOR PRIOR APPLICATION ADDICATION DATE: 2001-06-26
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Best Local Similarity 100.0%; Pred. No. 5.7e-59;
Matches 116; Conservative 0; Mismatches 0; Indels
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Publication No. US20040009480A1
GENERAL INFORMATION:
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Malyankar, Uriel M.
Millet, Isabelle
Padigaru, Muralidhara
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US-10-162-335-82
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APPLICANT: Pena, Carol E. A. APPLICANT: Rastelli, Luca APPLICANT: Rastelli, Luca APPLICANT: Shimkets, Richard A. APPLICANT: Shome, David J. APPLICANT: Stone, David J. APPLICANT: Vernet, Corinne A. M. APPLICANT: Vernet, Corinne A. M. APPLICANT: Vernet, Corinne A. M. APPLICANT: Zerhusen, Bryan D. TITLE OF INVENTION: Therappeutic Polypeptides, Nucleic Acids Encoding Same, FILE REFERENCE: 21402-377 B CURRENT APPLICATION NUMBER: US/10/162,335 CURRENT FILING DATE: 2002-10-01
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PRIOR APPLICATION NUMBER: 06/295,607

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-06

PRIOR PILING DATE: 2001-06-12

PRIOR PILING DATE: 2001-06-11

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PRIOR PILING DATE: 2001-06-12

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-16

PRIOR PILING DATE: 2001-06-16

PRIOR PILING DATE: 2001-06-17

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284 AGKKYPIDFVARETTCSKESNEELTESCETKKLGGSLDCNAEVYVVPWEKKIYPTV 339
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Best Local Similarity 100.0%; Pred. No. 1.1e-58;
Matches 116; Conservative 0; Mismatches 0;
                                                                                                                                                                                             Application US/10162335
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Hjalt, Tord
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Malyankar, Uriel M.
Millet, Isabelle
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Gangolli, Esha A.
Gerlach, Valerie
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Gorman, Linda
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CORGANISM: Homo sapiens
US-10-162-335-74
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                                                  셤
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APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zerbusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method FILE REFERENCE: 21402-377 B
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CURRENT APPLICATION NUMBER: US/10/162,335
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-16
PRIOR APPLICATION NUMBER: 60/296,414
PRIOR PLING DATE: 2001-06-11
PRIOR PLING DATE: 2001-06-12
PRIOR PLING DATE: 2001-06-14
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-26
PRIOR PLING DATE: 2001-06-26
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Boldoy, Ferenc L.
Casman, Stacie J.
Bdinger, Shlomit R.
Gangolli, Esha A.
Gerlach, Valerie
Gorman, Linda
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Pena, Carol E. A.
Rastelli, Luca.
Shimkets, Richard A.
Stone, David J.
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Padigaru, Muralidhara
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MacDougall, John R.
Malyankar, Uriel M.
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                                                                                                                                                                                                                                          APPLICANT: Anderson, David W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application NUMBER OF SEQ ID NOS: 201 SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-72
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and Method

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63 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                             313 AGKKYFIDFVARETICSKESNEELTESCETKKIGGSLDCNAEVYVVPWEKKIYPTV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AGKKYFIDFVARETTCSKESNEBLTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
55.5%; Score 381; DB 14; Length 4;
Best Local Similarity 62.1%; Pred. No. 5.8e-33;
Matches 72; Conservative 14; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Teccin, ward,
APPLICANT: Wang, Feng
APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
TITLE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
SEQ ID NO 217
LENGHIA 424
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APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8665%
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CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR PILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 215
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Procter & Gamble Company APPLICANT: Peters, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 215, Application US/10316253
Publication No. US20030162706A1
GENERAL INFORMATION:
PPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
APPLICANT: Thompson, Larry
                                                                                                                                                                                                                                                                                                                  Sequence 217, Application US/10316253; Publication No. US20030162706A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-217
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; ORGANISM: Rattus norvegicus
US-10-316-253-215
                                                                                                                                                                                                                                                                                          US-10-316-253-217
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APPLICANT: SEVER'S Kimberly A.
APPLICANT: SEVER'S COTING A.
APPLICANT: Vernet, Coring A.
APPLICANT: Vernet, Coring A.
APPLICANT: Vernet, Coring A.
APPLICANT: Vernet, A.
APPLICANT: Vernet, A.
APPLICANTON TOWNERS: US 1001-05-01
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method CURRENT APPLICATION NUMBER: US 1010-05-01
PRIOR APPLICATION NUMBER: 06/295,601
PRIOR APPLICANTON NUMBER: 06/295,601
PRIOR PRILING DATE: 2001-05-01
PRIOR PLILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: 60/299,557
PRIOR PLILING DATE: 2001-05-12
PRIOR APPLICANTON NUMBER: 60/299,555
PRIOR APPLICANTON NUMBER: 60/299,556
PRIOR PLILING DATE: 2001-05-16
PRIOR PLILING DATE: 2001-05-16
PRIOR PLILING DATE: 2001-05-16
PRIOR APPLICANTON NUMBER: 60/299,556
PRIOR APPLICANTON NUMBER: 60/299,556
PRIOR PRICR PLILING DATE: 2001-05-16
PRIOR PLILING DATE: 2001-05-
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                                                            313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVPWEKKIYPTV 368
                          63 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTV 118
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                                                                                                                                                                                                                                           Sequence 84, Application US/10162335 Publication No. US20040009480A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Baumgartner, Jason C.
Boldog, Ferenc L.
Casman, Stacie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edinger, Shlomit R. Gangolli, Esha A. Gertach, Valerie Gorman, Linda Guo, Xiaojia (Sasha) Hjalt, Tord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Millet, Isabelle
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patturajan, Meera
Pena, Carol E. A.
Rastelli, Luca
Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MacDougall, John R. Malyankar, Uriel M.
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, David W. APPLICANT: Baumgartner, Jaso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-10-162-335-84
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Best Local Similarity
Matches 116; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 FVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

23.8%; Score 163.5; DB 10; Length 167;
Best Local Similarity 31.6%; Pred. No. 1.2e-09;
Matches 37; Conservative 22; Mismatches 45; Indels 13;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISCHRATION NUMBER: 46,931
TELEPHONE: (617) 22277400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,834
FILING DATE: 01-Oct-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/471,765
FILING DATE: «Unknown»
APPLICATION NUMBER: US/08/791,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | LENGTH: 167 amino acids
| TYPE: amino acids
| TYPE: amino acid
| STRANDEDNESS: <UNKnown>
| POPOLOGY: linear
| MOLECULE TYPE: protein
| SEQUENCE DESCRIPTION: SEQ ID NO: 197:
| US-09-746-783-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: <Unknown>
APPLICATION NUMBER: 09/471,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09969834 Patent No. US20020102711A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                   11 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 70
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                   3 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 VEIGRITCKKNOHIRL-DDCDFQINHTLKQILSCYSEVWVVPW-----LQHFE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 FVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVTVNHWE 124
                                                                                                                                                                                                              Gaps
                                                                                                                                                                      63 AGKKYPIDFVARETICSKESNEELTESCETKKIGOSLDCNAEVYVVPWEKKIYPTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Indels 13;
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MCCOy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
Entrol N. SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%; Score 163.5; DB 1.
31.6%; Pred. No. 9.7e-10;
tive 22; Mismatches 45
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-329-428-2, Seplication US/10329428
Publication No. US20030114646A1
GENERAL INFORMATION:
I TITLE OF INVENTION: Human Cystatin F
FILE REFRENCE PF265P1D2
CURRENT APPLICATION NUMBER: US/10/329,428
CURRENT FILING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: 08/832,535
PRIOR APPLICATION NUMBER: 08/832,535
PRIOR FILING DATE: 1996-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PARENTH VERSION 3.2
SOFTWARE: PARENTH VERSION 3.2
SOFTWARE: PARENTH VERSION 3.2
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Best Local Similarity 31.61
Matches 37; Conservative
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. US20020137671A1

PAPLICANT: University of British Columbia

TITLE OF INVENTION: Production and use of Modified Cystatins

FILE REFERENCE: 58065

CURRENT PLING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: CA99/00717

PRIOR APPLICATION NUMBER: 60/095,503

PRIOR PILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-05

WUMBER OF SEQ ID NOS: 32
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Patent No. US20020137671A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of British Columbia
TITLE OF INVENTION:
FILE REPRENENT S8069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                        Query Match 23.7%; Score 163; DB 9; Length 178; Best Local Similarity 34.0%; Pred. No. 1.4e-09; Matches 35; Conservative 20; Mismatches 44; Indels
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PF-0193 US
                                                                                                                                                                                                                                                  CLONE: 30443
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-969-834-1
               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                  LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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US-09-775-932-14
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Best Local Similarity
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US-09-775-932-12
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Publication No. US20030221209A1
GENERAL INFORMATION:
APPLICANT: Atkinson, Howard J.
APPLICANT: McPherson, Michael J.
APPLICANT: Urwin, Peter E.
TITLE OF INVENTION: MODIFIED PROTEINASE INHIBITORS
UNWERSPONDENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        20.2%; Score 138.5; DB 9; 31.5%; Pred. No. 4.5e-07; iive 22; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION US/09940497
FRICANT: Ni et al.
TITLE OF INVENDATION:
TITLE OF INVENTION: Human Cystatin E
TITLE FERENCE: PF202P102
CURRENT APPLICATION NUMBER: US/09/940,497
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/241,376
PRIOR FILING DATE: 1999-02-02
PRIOR FILING DATE: 1996-06-05
PRIOR FILING DATE: 1995-06-05
                                   1999-08-05
MBER: 60/095,503
PRIOR APPLICATION NUMBER: CA95;
PRIOR FILING DATE: 1999-08-05;
PRIOR APPLICATION NUMBER: 60/6;
PRIOR FILING DATE: 1998-08-05;
NUMBER: OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.0
                                                                                             1998-08-05
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.54
Matches 34; Conservative
                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 34; Conserv
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ADDRESSEE: Klauber & Jackson
CITY: Hackensack Avenue, 4th Floor
COMPUTE: USA
COMPUTE: USA
COMPUTE: USA
COMPUTE: Plopy disk
COMPUTE: Plopy disk
COMPUTE: Plopy disk
COMPUTE: Labarin Process
COMPUTE: Labarin Action
COMPUTE: Labarin Acti
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Search completed: September 24, 2004, 14:13:04 Job time : 45.704 secs

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Query Match

90.9%; Score 600; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 112; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 720 KD
COMPUTER: Diskette, 3.50 inch, 720 KD
COMPUTER: BW F8/2
COMPUTER: BW F8/2
COMPUTER: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US, Application
FILING DATE: 9 February 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: WS, Application
APPLICATION NUMBER: Serial No. 5472945 07/744,545
FILING DATE: 13 August 1991
ATTORNEY AGENT INPORMATION:
NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 6056-137 CII
TELECOMMUNICATION INPORMATION:
TELEPHONE: (215) 568-8383
TELER: No. 54729456
TELER: No. 54729456
TELER: No. 54729456
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
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peptide
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; TOPOLOGY:
US-08-193-114B-1
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445.051 Million cell updates/sec
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Sequence 2,
Sequence 3,
Sequence 9,
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/edforcoMB.pep:*
/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-019-485-3
US-09-617-302-9
US-09-617-302-9
US-08-676-242-11
US-08-676-242-11
US-09-475-932-14
US-09-775-932-14
US-08-441-186-2
US-08-441-186-2
US-08-441-186-2
US-08-431-480-8
US-09-431-480-8
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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Perfect score:
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                                                                                       Run on:
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Sequence 19, Appl Sequence 46, Appl Sequence 48, Appl Sequence 93, Appl Patent No. 5432264 Sequence 26, Appl Sequence 5, Appl Sequence 18, Appl Sequence 11, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli	of Platelet Activation
1127 4 US-08-849-303-19 1140 4 US-09-886-319A-46 1140 4 US-09-886-319A-46 1140 4 US-09-599-360B-93 111 4 US-09-599-360B-93 110 4 US-09-75-932-2 1140 3 US-09-617-302-5 1140 4 US-09-775-932-5 1140 4 US-09-775-932-5 1140 4 US-09-775-932-1 1145 2 US-08-832-535-11 1146 3 US-09-919-485-4 1146 3 US-09-919-485-4 1146 3 US-09-919-485-4 1146 3 US-09-911-480-6 1146 3 US-09-911-480-6 1146 3 US-09-911-480-6 1146 3 US-09-617-302-6	LIGNMENTS B of Blood d Inhibition gen Fragment orgna &
28 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 129.5 19.6 19.6 19.6 19.6 19.6 19.6 19.6 19.6	RESULT 1 US-08-193-114B-1 US-08-193-114B-1 Sequence 1, Application US/08193114 Sequence 1, Application US/08193114 Sequence 1, Application Sequence 1 TYPLE OF INVENTION: Modulation TITLE OF INVENTION: Pressure an TITLE OF INVENTION: With Kinino NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Seidel, Gonda, Lav ADDRESSEE: Reidel, Gonda, Lav STREET: 1880 TWO Penn Center CITY: Philadelphia STREET: Pennsylvania

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GENERAL INFORMATION:
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                                         1 CVGCPRDIPTNSPELEETLTHTITKLNAENNAFFFKIDNVKKARVQVVAGKKXFIDFVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                       72 RETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLGM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9206809
GENERAL INFORMATION:
APPLICANT: Schmaier, Alvin H.
APPLICANT: Jiang, Yongping
TITLE OF INVENTION: Modulation of Blood
TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Commonwealth System of Higher Education
STREET: 406 University Services
STREET: Building
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.0%; Score 594; DB 5; Best Local Similarity 98.2%; Pred. No. 2.7e-58; Matches 110; Conservative 2; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KD
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: WordDerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06809
FILING DATE: 19910813
CLASSIFICATION DATA:
APPLICATION NUMBER: Serial No. 744,545
FILING DATE: 13 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 117 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
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RESULT 3 18-08-791-522-1 'Sequence 1, Application US/08791522 'Patent No. 5935817

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1. Application US/09314777

Sequence 1. Application US/09314777

Fatent No. 6110686

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.

ITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
ADDRESSEE: ACQUENCES: 4

CORRESPONDENCE ADDRESSE:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Forter Drive

CITY: Palo Alto

STREET: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,522
FILING DATE: Filed Herewith
FRIOR APPLICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TILING DATE:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0193 US
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NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-855-055
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 amino acids
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STRANDEDNESS: single
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IMMEDIATE SOURCE:
CLONE: 30443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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GENERAL INFORMATION:
APPLICANT: Li, Hacdong
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Ni, Jian
TITLE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09019485 Patent No. 6066617
TELEPHONE: (201) 994-1700
TELEPAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 145 amino acids
amino acid
                                                                                                        | LENGTH: 145 amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| MOLECULE TYPE: protein
| US-08-832-535-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-019-485-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 FVARETICSKESNEELIESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVN--CQPLGM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
25.6%; Score 169; DB 3; Length 178;
Best Local Similarity 32.5%; Pred. No. 5.4e-11;
Matches 39; Conservative 22; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,535 FILING DATE: 03-APR-1997 CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2. Application US/08832535
; Sequence 2. Application US/08832535
; Patent No. 5919658
; GENERAL INFORMATION:
    APPLICANT: N. JIAN
    APPLICANT: LI, HADDONG
; APPLICANT: TU, GUO-LIANG
    APPLICANT: YU, GUO-LIANG
    APPLICANT: GENTZ, REINER L
    TITLE OP INVENTION: HUMAN CYSTATIN F
    NUMBER OF SEQUENCES: 1
    CORRESPONDENCE ADDRESS:
    ADDRESSE: ADDRESSE:
    ADDRESSE: HUMAN GENOME SCIENCES, INC.
    STREET: 9410 KEY WEST AVENUE
    CITY: ROCKVILLE
    STREET: WD
    CONTRE: WD
    CONTRE: WD
    CONTRE: WD
     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,522
FILING DATE:
ATTONEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELEPHONE: 415-85-055
TELEPHONE: 415-845-416
INFORMATION POS EDG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acid
TYPE: Amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,610
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NAME: KIMBALL, PAUL C.
REGISTRATION NUMBER: 34,61C
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-314-777-1
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9 TKICVGCPRDIPINSPELEETLIHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 68
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                                                                                                                                                                                                                                                                                                 32 SRVKPGPPKTIKTNDPGVLQAARXSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 VEIGRITICKKNOHLRL-DDCDFQINHTLKQTLSCYSSVWVVPWLQHFBVPVLRC 144
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Query Match 25.1%; Score 165.5; DB 2; Length 145; Best Local Similarity 32.5%; Pred. No. 1e-10; Matches 37; Conservative 22; Mismatches 50; Indels 5;
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FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BENSON, ROBERT H.
REFERENCE/DOCKET NUMBER: PF265F1
TELECOMMUNICATION INFORMATION:
TELEFRAM: 301309854
TELEFRAM: 301309854
TELEFRAM: 3013098439
TELEFRAM: ASSTEMITION:
TELEFRAM: ASSTEMITI
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1e-10;
50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Human Genome Sciences, Inc. STREE: 9410 Key West Avenue CITY: Rockville STATE: MD
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9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYPID 68
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69 FVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC 118
                              92 VEIGRITCKKNQHLRL-DDCDFQTNHTLKQTLSCYSEVWVVPWLQHFEVPVLRC 144
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Patent No. 6235708

GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaway, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72

CURRENT APPLICATION NUMBER: US/09/431,480

CURRENT FILING DATE: 1999-11-01

EARLIER APPLICATION NUMBER: 60/109,217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                              APPLICANT: Li, Haodong
APPLICANT: Yu, Guo-Liang
APPLICANT: Grantz, Reiner
APPLICANT: Ni, Jian
TITLE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                             Sequence 3, Application US/09019485
Patent No. 6066617
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERSON, ROBERT H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF26:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 32.5
Matches 37; Conservative
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MOLECULE TYPE: protein
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US-09-431-480-9
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9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 68
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Fatent No. 6245529
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72
CURRENT FILING DATE: 2000-07-17
CURRENT FILING DATE: 2000-07-17
FRICE APPLICATION NUMBER: 09/431,480
FRICE RELING DATE: 1999-11-01
FRICE PRINCE DATE: 1999-11-20
FRICE PRINCE APPLICATION NUMBER: 60/109,217
FRICE FILING DATE: 1999-11-20
FRICE RELING DATE: 1999-11-20
FRICE RELING DATE: 1999-10-26
FRICE RELING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                          25.1%; Score 165.5; DB 3; 32.5%; Pred. No. 1e-10;
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Patent No. 6576745
GENERAL INFORMATION:
APPLICANT: Li, et al.
ITILE OF INVENTION: Human Cystatin F
FILE REFERENCE: PF265FD10
CURRENT APPLICATION NUMBER: US/09/528,436B
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/019,485
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: 60/156,382
EARLIER FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 32.5$
Warches 37; Conservative
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Matches 37; Conservative
                                                                                                                                                     LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-617-302-9
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TYPE: PRT
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                                                                                                                                  SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                         92 VEIGRITCKKNQHLRL-DDCDFQINHTLKQTLSCYSEVWVVWMLQHPEVPVLRC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Bradykinin OTHER INFORMATION: analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                         Length 145;
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23.5%; Score 155; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         50; Indels
                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                         25.1%; Score 165.5; DB ilarity 32.5%; Pred. No. 1e-10; Conservative 22; Mismatches
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PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: 08/832,535
PRIOR FILING DATE: 1999-04-03
PRIOR APPLICATION NUMBER: 60/014,795
PRIOR FILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PARENTIN VERSION 3.2
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08676242C Patent No. 6143719 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-528-436B-2
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Best Local Similarity
Matches 37; Conserva
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US-08-676-242-22
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US-08-676-242-11
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                                                                                                                                               TYPE: PRT
                                                                                                                                  LENGTH:
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Sequence 22, Application US/08676242C
Sequence 22, Application US/08676242C
Patent No. 6143719
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THOROGENIS OF the University of Michigan
APPLICANT: Schmaier, Alvin H.
APPLICANT: Hasan, Ahmed A.K.
TITLE OF INVENTION: Brachytinin Analogs As Selective Thrombin Inhibitors
FILE REPERBNCE: 8820-2 US
CURRENT APPLICATION NUMBER: US/08/676,242C

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APPLICANT: Schmainer, Alvin H.
APPLICANT: Hasan, A.K. Ahmed
TITLE OF INVENTION: Bradykinin Analogs As Selective Inhibitors of Cell
TITLE OF INVENTION: Activation
FILE REFERENCE: 8820-3
CURRENT APPLICATION NUMBER: US/09/402,732
CURRENT APPLICATION NUMBER: 06/046,085
PRIOR APPLICATION NUMBER: 60/046,085
PRIOR APPLICATION NUMBER: PCT/US98/08015
PRIOR PILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 64
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OTHER INFORMATION: Description of Artificial Sequence: From human
OTHER INFORMATION: Kininogen heavy chain
1. OTHER INFORMATION: Kininogen heavy chain
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Sequence 14, Application US/09775932
Patent No. 653477
GENERAL INFORMATION:
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR PLICATION NUMBER: CA99/00717
PRIOR PLILING DATE: 1999-08-05
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22.0%; Score 145; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.0%; Score 145; DB 3; I
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 25; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2000-07-16
EARLIER APPLICATION NUMBER: 66/000,096
EARLIER FILING DATE: 1995-6-09
EARLIER FILING DATE: 1996-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-775-932-14
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8 PTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFI 67
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US-09-775-932-12
Sequence 12, Application US/09775932
Sequence 12, Application US/09775932
Sequence 12, Application US/09775932
Sequence 12, Application US/09775932
SEQUENCE INFORMATION:
SETLE OF INVENTION:
Production and use of Modified Cystatins
TITLE OF INVENTION:
PRIOR REFERENCE: 58069
CURRENT FILING DATE: 1090-102-02
PRIOR APPLICATION NUMBER: US/09/775,932
PRIOR APPLICATION NUMBER: CA99/00717
PRIOR APPLICATION NUMBER: 60/095,503
PRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 12
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                               68 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 109
                                                                                                                                                                                                                              Query Match
21.0%; Score 138.5; DB 4; Length 121;
Best Local Similarity 31.5%; Pred. No. 7.7e-08;
Matches 34; Conservative 22; Mismatches 45; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TWEMGSTDCRKTRVTGDHVDLT-TCPLAAGAQQEKLRCDFEVLVVPWQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.0%; Score 138.5; DB 4; Length 128, Best Local Similarity 31.5%; Pred. No. 8.3e-08; Matches 34; Conservative 22; Mismatches 45; Indels 7
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PRIOR APPLICATION NUMBER: 60/095,503
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 121
                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-775-932-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-932-12
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OM protein - protein search, using sw model

September 24, 2004, 14:02:27; Search time 49.692 Seconds (without alignments) 699.375 Million cell updates/sec Run on:

US-10-661-784-1 660

1 GKDFVQPPTKICVGCPRDIP.......YVVPWEKKIYPTVNCQPLGM 123 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp2003as:* A_Geneseq_29Jan04:* geneseqp1990s:*geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description		Abp70801 Human ext	1799	Abu92044 Human pro		Abu99149 Novel hum	Abu99143 Novel hum	Ade76864 Human pro	44 Novel	Ниша	Abg21101 Novel hum	Human		Abu99145 Novel hum	Aab37447 Human kin		Abg21105 Novel hum	Aap40257 Bradykini		Aap40633 Bradykini	77		Abg21099 Novel hum	Abg21100 Novel hum	Mouse
ΩI	AAY95426	ABP70801	ABP70799	ABU92044	ABP70800	ABU99149	ABU99143	ADE76864	ABU99144	ABB78707	ABG21101	ABB78710	ABU99150	ABU99145	AAB37447	AAR33350	ABG21105	AAP40257	ABR41202	AAP40633	ABG60077	ABG21102	ABG21099	ABG21100	AAW98907
DB	m	v	9	9	Q	Q	G	æ	w	ഗ	4	ഗ	ø	G	m	N	4	-1	9	ч	2	4	4,	4	ď
% Query Match Length	~	304	322	329	358	390	398	427	615	626	644	644	644	4	122	117	435	436	357	434	235	248	369	305	167
% Query Match	0	100.0	00	100.0		100.0	100.0	100.0	100.0		100.0	00		00		90.0								28.8	26.5
Score	9	099	660	9	660	660	099	099	660	099	099	660	099	099	628	594	589.5	477	453	450	409	320.5	316	190	175
Result No.	н	7	m	4	2	φ	7	۵۵	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aaw69734 Human cys	Aay95418 Anti-angi	Aab37445 Human cys	Aaw32323 Mature hu	Aaw31902 Human cys	Aay25708 Human cys	Human	Aae04439 Human.cys	Add14098 Human src	Aay02287 Secreted		Aay95408 Anti-angi	Aab37446 Human kin	Aaw98910 Mouse IMC	Aaw54335 Bradykini	Aay95425 Anti-angi	Aaw54341' Bradykini	Aaw77418 Kininogen	Aay81200 Human mut	Aay81189 Human mut
AAW69734	AAY95418	AAB37445	AAW32323	AAW31902	AAY25708	AAE02410	AAE04439	ADD14098	AAY02287	ADA45154	AAY95408	AAB37446	AAW98910	AAW54335	AAY95425	AAW54341	AAW77418	AAY81200	AAY81189
178 2			145 2				145 4	145 7	167 2	167 7	32 3	122 3		27 2	27 3	4		121 3	128 3
25.6	25.2	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	24.4	23.8	23.7	23.5	23.2	22.0	22.0	21.9	21.9
169	166	165.5	165.5	165.5	165.5	165.5	165.5	165.5	165.5	165.5	161	157	156.5	155	153	145	145	144.5	144.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY95426 standard; peptide; 123 AA RESULT 1 AAY95426

25-SEP-2000 (first entry)

Human high mol.wt. kininogen domain 3.

Anti-angiogenic; anglogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.

Homo sapiens.

WO200035407-A2.

22-JUN-2000

99WO-US028465. 02-DEC-1999; 98US-0112427P. 16-DEC-1998;

(UTEM) UNIV TEMPLE. (MCCR/) MCCRAE R K.

Mccrae RK;

WPI; 2000-442247/38.

Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3

Disclosure; Page 4; 44pp; English.

The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention provides peptides (see AAY95405-24) that are analogues of certain sites in the HK domain 3, specifically Abn275-Iys282, Cy5246-Cy5249, Leu31-Tyr338 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit apothehial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer,

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Gaps

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Human, extracellular messenger, EXMES; cytostatic; antidiabetic;
immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
endocrine disorder; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NW, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS; Khare R, Wilson AD, Uin P, Hawkins PR, Tang YT, Burford N; Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y; on TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;
                                                                                                                                                                                                                                  130 GKDFVQPPTKICVGCPRDIPTNSPELEBTLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                  AGKKY FID FVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
                                                                                                                                                                                                                                                                                                        190 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
                                                                                                                                                                                                          1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
       for diagnosing or treating a disease or condition associated with. decreased expression or overexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or
                                                                                                                                  100.0%; Score 660; DB 6; Length 3 100.0%; Pred. No. 8e-66; ive 0; Mismatches 0; Indels
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14-DEC-2001; 2001US-0340584P.
18-DAN-2002; 2002US-0350595P.
11-MAR-2002; 2002US-0363432P.
15-MAR-2002; 2002US-03646CPP.
05-ARR-2002; 2002US-0370761P.
24-UUN-2002; 2002US-0391378P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extracellular messenger,
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Richardson TW, Kable AE,
                                                                                                                                                                         Matches 123; Conservative
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N-PSDB; ACC42386.
                                                                                                                                                         Similarity
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                                                                                                   AA;
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                                                                                                   Sequence 304
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                                                                                                                                    Query Match
Best Local 9
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immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
endocrine disorder; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duggan BM, lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS;
Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;
Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y,
Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human extracellular messenger (EXMES) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional EXMES e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel human extracellular messenger proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences (ACC42361-ACC42388). The proteins are useful for preparing a composition
                                                                                                                                                                                     AGKKYPIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
                                                                                                                                                                                                                                                                 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
rheumatoid arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated
                                                                                                                                                               1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                    Gaps
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                                                                                             Length 123;
                                                                                                                                Indels
                                                                                       100.0%; Score 660; DB 3;
100.0%; Pred. No. 2.3e-66;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human extracellular messenger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-2001; 2001US-0314811P.
14-DEC-2001; 2001US-0340584P.
18-JAN-2002; 2002US-0350595P.
11-MAR-2002; 2002US-0363432P.
15-MAR-2002; 2002US-0364607P.
05-APR-2002; 2002US-037661P.
24-JUN-2002; 2002US-0391378P.
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                                                                                       Cuery Match
Best Local Similarity 100.
Matches 123; Conservative
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N-PSDB; ACC42388.
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                                                    Sequence 123 AA;
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Homo

RESULT 2

JD ABP70801

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KW Hum

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The present invention relates to novel human extracellular messenger

Claim 1; Page 205-206; 224pp; English.

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207
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proteins (EXMES-1 to-28, ABP70774-ABP70801) and their coding sequences (ACG42361-ACC42388). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or over-expension of functional EXMES e.g. autoimmune/inflammatory disorderes, diabetes, endocrine disorders or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allorgy; inflammatory disorder; Allos; developmental disorder; hypothyroidism; Cushing's syndrome; gastrointestinal disorder; epithelial disorder; infection; ortostatio; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic.
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                                                                                                                                                                                                                                                                                                                  208 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
                                                                                                                                                                                                                            1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                         148 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee S:
Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;
Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE,
Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;
Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein modification and maintenance molecule-24 (PMMM-24).
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                                                                                                                                                         Length 322;
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                                                                                                                                                       100.0%; Score 660; DB 6;
100.0%; Pred. No. 8.7e-66;
ive 0; Mismatches 0;
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25-OCT-2001; 2001US-0335703F.
09-NOV-2001; 2001US-0348887F.
28-NOV-2001; 2001US-0334145F.
06-DEC-2001; 2001US-0337451F.
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                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 123; Conservative
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                                                                                                                        Sequence 322 AA;
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                                                                                         cancer
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The present invention relates to the isolation of human protein

modification and maintenance molecules (PMMM), and the polymucleotide
sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM-10 between them. A total of 40 PMMM polypeptides (designated PMMM-10 condition or disease associated with the expression of PMMM in a subject, preparing a polyclonal or monoclonal antibody, and generating an expression profile of a sample containing the polymucleotides. The diseases or conditions associated with decreased cypmucleotides. The diseases or conditions associated with decreased cypmucleotides. The disease or conditions associated with decreased cypmucleotides. The disease, stroke), immune/inflammatory disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergides), developmental disorders (e.g. hypochyroidism, Cubaling's syndrome), gastrointestinal or epithelial disorders, and infections. The PMMM polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or anteagonists of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to, or modulate the activity of the polypeptide.

ABU92021-ABU92060 represent the human PMMM polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; extracellular messenger; EXMES; cytostatic; antidiabetic; immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes; endocrine disorder; cancer.
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or
aberrant PMMM expression e.g. cancer, atherosclerosis,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human extracellular messenger, EXMES-27.
                                                         Claim 1; Page 264-265; 311pp; English
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14-DEC-2001; 2001US-0340584P.
18-QAN-2002; 2002US-0350595P.
11-MAR-2002; 2002US-0363450P.
15-MAR-2002; 2002US-036460PP.
05-APR-2002; 2002US-0370761P.
24-UUN-2002; 2002US-0391378P.
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Best Local Similarity
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04-JUN-2002; 2002WO-US017428

14-JUN-2001, 2001US-0298285P. 15-JUN-2001, 2001US-029856F. 21-JUN-2001, 2001US-029949P. 26-JUN-2001, 2001US-0300883P. 28-JUN-2001, 2001US-0301S50P. 13-AUG-2001; 2001US-0311S972P.

29-AUG-2001; 2001US-0315660P 14-SEP-2001; 2001US-0322293P 17-SEP-2001; 2001US-0322706P

2002US-0363673P 2002US-0363676P 2002US-00363676

28-FEB-2002; 12-MAR-2002; 14-DEC-2001;

(CURA-) CURAGEN CORP.

03-JUN-2002;

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                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel human extracellular messenger proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences (ACC42361-ACC42388). The proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional EXMES e.g. autoimmune/inflammatory disorders, diabetes, endocrine disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                New human extracellular messenger (EXMES) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional EXMES e.g. autoimmune disorders or cancer.
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                                         BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS; Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N; Yao MG, Becha SD, Tran UK, Chien D, Zebarjadian Y, son TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 206; 224pp; English.
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INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                WPI; 2003-278643/27.
N-PSDB; ACC42387.
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                                                                                                                                      Ramkumar J;
                                                                                                                Richardson
                                            Duggan BM,
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New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

Claim 1; Page 147; 332pp; English.

pharmacogenomics

FL, Casman SJ, Edinger SR; Guo X, Hjalt T, Kekuda R, Li L; I, Padigaru M, Patturajan M; Stone DJ, Spytek KA, Vernet CAM;

Anderson DW, Baumgartner JC, Boldog FL, Casman Gangolli EA, Gerlach VL, Gorman L, Guo X, Hj: Macdougall JR, Malyankar UM, Millet I, Padiga: Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Voss EZ, Zerhusen BD;

2003-140627/13 WPI; 2003-140627, N-PSDB; ACD03653

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The invention describes an isolated polypeptide (I) comprising any of 27 118-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology syndrome associated with the polypeptide. The Novx polypeptides, polynucleotides and antibodies are useful in treating or preventing NoVx-associated disorders, and cathority, atherosclerosis, cancer, passociated cachexia, and other wasting disorders, parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated value for the identification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, call proliferation, haematopolesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NoVx substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hypridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein
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100.0%; Score 660; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.1e-65;
Matches 123; Conservative 0; Mismatches 0;
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cell proliferation, haematopoiesis, wound healing, angiogenesis, chromosome mapping, tissue typing; preventive medicine; pharmacogenomic.

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12-DEC-2002

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pharmacogenomics.
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            276 AGKKYFIDFVARETTCSKESNBELTESCETKKLGQSLDCNAEVIVVPWEKKIYPIVNCQP 335
                                                                                                                                                                                                              Human; G-protein coupled receptor related protein; GPCR related protein, NOV; cytostatic; ardiant; antiatteriosclerotic; antidiabetic; immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; antiparkinsonian; neuroprotective; nociropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; diabetes; immune disorder; AIDS; obesity; asthmatic; haematopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; estimatopoietic; chonce disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; anglogenesis; cell differentiation; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR; Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L; Macdougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M; Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CAM; Voss EZ, Zerhusen BD;
                                                                                                                                                                                             Novel human GPCR related protein NOV12a.
                                                                                                                          ABU99143 standard; protein; 398 AA.
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15-UN-2001; 2001US-029856F.
26-UNN-2001; 2001US-0299949P.
28-UN-2001; 2001US-0300883P.
13-AUG-2001; 2001US-0311972P.
27-AUG-2001; 2001US-0311972P.
29-AUG-2001; 2001US-0311972P.
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17-SEP-2001; 2001US-0322706P.
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14-DEC-2001; 2001US-0341186P.
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2002US-0363673P,
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03-JUN-2002; 2002US-00363676.
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                                                                                                                                                                      (first entry)
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                                            LGM 123
                                                                   IGM 338
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                       01-AUG-2003
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                                                                                                                                                ABU99143;
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The invention describes an isolated polypeptide (I) comprising any of 27 (18-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 * identical to them, or a sequence having one or more conservative substitutions in them. The collypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NoVX polypeptides, polymolocities and antibodies are useful in treating or preventing NoVX-associated disorders, e.g. cardiomyopathy, atherosolerosis, cancer, discase, Alzheimer's disease, infections, multiple sclerosis, cancer. C discase, Alzheimer's disease, infections, multiple sclerosis, cancer associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, contibodies that bind immunospecifically to NoVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as targets or the contibodies that bind immunospecifically to NoVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as vaccines. This is the amino acid sequence of a novel human G-protein NoVX value of a p
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100.0%; Score 660; DB 6; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 123; Conservative 0; Mismatches 0; Indels
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Claim 1; Page 143; 332pp; English.
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WO200299116-A2

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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type I diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of secretary several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to commulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid is sequence of a protein encoded by a cDNA differentially expressed in a
                                                                                                      Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver disorders.
                                                                                                                                                                                                                     Claim 1; SEQ ID NO 29; 41pp; English.
                       WPI; 2004-031227/03.
N-PSDB; ADE76863.
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Sequence 427 AA;

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253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312
                                                                                                                                                                    61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
                                                                                                                                                                                          313 AGKKYFIDFVARETTCSKESNEELTESCETKKIGGSLDCNAEVYVVPWEKKIYPTVNCQP 372
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                                                                                    1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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  Query Match 100.0%; Score 660; DB 8; Length 427; Best Local Similarity 100.0%; Pred. No. 1.3e-65; Matches 123; Conservative 0; Mismatches 0; Indels (
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LGM 375
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ABU99144 standard; protein; 615 AA. 01-AUG-2003 ABU99144; ABU99144
ID ABU9
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AC ABU5
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DT 01-2
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KW Hum
KW NOV
KW IMM
KW ADD
KW RESULT 9

(first entry)

Novel human GPCR related protein NOV12b.

Human, G-protein coupled receptor related protein; GPCR related protein; NOV, cytostatic, cardiant, antiarteriosclerotic, antidiabetic; immunodulator; anti-HIV; anocetic, antiasthmatic, hemostatic; antiparkinsonian, neuroprotective; nootropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; NOVX-associated disorder; AIDS; Obesity; asthma; haematopoietic disorder; AIDS; Obesity; asthma; haematopoietic disorder; Parkinson's disease; AIDS; infection; multiple sclerosis; cancer-associated cachexia; disease; infection; multiple sclerosis; cancer-associated cachexia; call differentiation; cell proliferation; haematopoiesis; wound healing; anglogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

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Length 615; Indels

100.0%; Score 660; DB 6; 100.0%; Pred. No. 2.1e-65; ive 0; Mismatches 0;

Conservative

Local Similarity es 123; Conserv

Query Match Best Loca Matches

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The invention describes an isolated polypeptide (I) comprising any of 27 [18-961 residue amino acid sequences, given in the specification, a macure form of them, a sequence that is at least 95 # identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardingwopathy, atherosciences, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardingwopathy, atherosciences, cancer. disorders, AlDS, obesity, asthma, haematopoietic disorders, Parkinson's disease, AlDs as a sociated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therappy, in generation of the rapeutic or diagnostic methods. The nucleic acids are further used as therapeutic or diagnostic methods. The nucleic acids are further used as multipodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as vaccines. This is the amino acid sequence of a novel human G-protein and coupled receptor related protein NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR; Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T. Kekkuda R, Li L; Macdougall JR, Malyankar UW, Millet I, Padigaru M, Parturajan M; Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 144; 332pp; English.
                                                                                                                                                                                                                                                                         26-UUN-2001; 2001US-0300883F.
28-UUN-2001; 2001US-0301550F.
13-AUG-2001; 2001US-0311972F.
27-AUG-2001; 2001US-031560F.
14-SEP-2001; 2001US-03125293F.
                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-2001; 2001US-0322706P.
14-DEC-2001; 2001US-0341186P.
28-FEB-2002; 2002US-0361189P.
12-MAR-2002; 2002US-0363673P.
12-MAR-2002; 2002US-0363676F.
                                                                                                                                              04-JUN-2001; 2001US-029561P.
06-JUN-2001; 2001US-0296404P.
06-JUN-2001; 2001US-0296418P.
                                                                                                                                                                                                              14-JUN-2001; 2001US-0298285P
15-JUN-2001; 2001US-0298556P
21-JUN-2001; 2001US-029949P
                                                                                   04-JJN-2002; 2002WO-US017428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pena CEA, Rastelli L,
Voss EZ, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
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The present invention describes an isolated polypeptide (I) that corresponds to the DS domain of human kininogen, or biologically active peptide fragment, homologue or functional derivative, and which: (a) inhibits anglogenesis; (b) binds to the DS binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis in EC; and/or (d) inhibits the signalling pathway required for maintenance of EC viability. (I) has cytostatic, antitumour, antiatherosclerotic, vasotropic, vulnerary, tranquilliesr, thrombolytic, ophthalmological, antiapoptocic and endocrine activities. An antiabody (IX) specific for an epitope of (I) is useful for inhibiting tumour growth or specific for an epitope of (I) and subject (II) or a dimeric or trimeric fusion polypeptide (III) can be used for inhibiting EC migration, proliferation, invasion, or angiogenesis, or for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X) comprising (I), (II), or (III), an be used for treating a subject having a disease or condition associated with undesired EC migration,
                                                                                           AGKKYPIDFVARETTCSKESNEELTESCETKKLGOSLDCNABVYVPWEKKIYPTVNCOP 343
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, kininogen, high molecular weight kininogen, HK, D5 domain, D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour; antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombolytic; ophthalmological; gynaecological; antiulcer; antidiabetic; antiatrhitic; antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
                    GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 283
                                                                        AGKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCOP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human kininogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign
  GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKINAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 13; 84pp; English.
                                                                                                                                                                                                                                                                                   ABB78707 standard; protein; 626 AA
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/label= D5 domain
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ATTE-) ATTENUON LLC.
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or (III) can be used mplex mixture and for
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                                                                                                                                                                                                                                                                                                         295 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVFWEKKIYPTVNCQP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
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proliferation, invasion or angiogenesis. (I), (II), or (III) can be use for isolating a D5 domain binding molecule from a complex mixture and fisolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the mature human high molecular weight kininogen (HK) procein, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                            235 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                         AGKKYPIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
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                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping, gene mapping, gene therapy, forensic, nedical imaging, diagnostic, genetic disorder.
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                                                                                                                                                    Length 626;
                                                                                                                                                                                     Indels
                                                                                                                                                    Score 660; DB 5;
Pred. No. 2.2e-65;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #21092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG21101 standard, protein, 644 AA.
                                                                                                                                                    100.0%;
larity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
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                                                                                                                                                                      Local Similarity
tes 123; Conserv
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                                                                                                                        Sequence 626 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human, kininogen, high molecular weight kininogen, HK; D5 domain, D5 receptor; angiogenesis; endothelial cell; cytostazic; antitumour; antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombolytic; ophthalmological; gynaecological; antiulcer; antidiabetic; antiatrhritic; antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
                                                                                                                                                                                                                            61 AGKKYFIDFVARETICSKESNEELIESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
        of sites expressing (II). (I) and (III) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
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 useful in medical imaging
                                                                                                                                                                                                  1 GKDFVQPPTKICVGCPRDIPTNSPELBETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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/label= mature_human_high_molecular_weight_kininogen
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                                                                                                                                                 Length 644;
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                                                                                                                                                100.0%; Score 660; DB 4;
100.0%; Pred. No. 2.3e-65;
(II) and its binding partners are
                                                                                                                                                                   Mismatches
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/label= signal
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/label= D5
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Matches 123; Conservative
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The present invention describes an isolated polypeptide (I) that corresponds to the D5 domain of human kininogen, or biologically active corresponds to the D5 domain of human kininogen, or biologically active peptide fragment, homologue or functional derivative, and which: (a) inhibits angiogenesis; (b) binds to the D5 binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis in EC; and/or (d) inhibits the signalling pathway required to maintenance of E viability. (3) has cytostatic, antitumour, antiatherosclerotic, vasocropic, valuerary, tranquilliser, thrombolytic, antiatherosclerotic, artiapoptotic and endocrine activities. An antibody (IX) specific for an epitope of (I) is useful for inhibiting tumour growth or angiogenesis in a subject. (1), a D5 fusion polypeptide (II) or a dimeric or trimeric fusion polypeptide (III) can be used for inducting EC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X) comprising (I), (II), or (III), can be used for treating a subject having a comparising (I), (II), or (III), can be used for reacting a subject having conferation, invasion or angiogenesis. (I), (II), or (III) can be used for isolating a D5 domain binding molecule from a complex mixture and for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the human high molecular when the breach invention which is given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372
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                                                                                                                                                                                                                                                                                          Novel human kininogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benigm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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100.0%; Pred. No. 2.3e-65;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1B-E; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU99150 standard; protein; 644 AA.
24-JUL-2000; 2000US-0220194P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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ses 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
                                                                                                                                                 Juarez JC;
                                                                          (ATTE-) ATTENUON LLC
                                                                                                                                                                                                                       WPI; 2002-393611/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 644 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    hyperplasia.
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                                                                                                                                                     Mazar AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The invention describes an isolated polypeptide (I) comprising any of 27 118-951 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 % identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a speciated with the polypeptide. The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardionyopathy, atherosclerosis, cancer, dabetes, immune disorders, AIDS, obesity, asthma, haematopoietic disorders, parkinson's secrited cachexia, and other wasting disorders packinson's disease. Allehemer's disease, infections, multiple solerosis, cancer-sessociated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or dispansortic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n SJ, Edinger SR;
alt T, Kekuda R, Li L;
ru M, Patturajan M;
Spytek KA, Vernet CAM;
diabetes; immune disorder; AIDS; obesity; asthma; haematopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; wasting disorder; chronic disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FL, Casman SJ,
Guo X, Hjalt T,
I, Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson DW, Baumgartner JC, Boldog FL, Casma Gangolli EA, Gerlach VL, Gorman L, Guo X, Hj Macdougall JR, Malyankar UM, Millet I, Padiga Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Voss EZ, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 148; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  26-UUN-2001, 2001US-0300883P
28-UUN-2001, 2001US-0301550P
13-UUG-2001, 2001US-031550P
29-AUG-2001, 2001US-031560PP.
                                                                                                                                                                                                                                                                                                                                    2001US-0296404P.
2001US-0296418P.
2001US-0298285P.
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2002US-0363673P.
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                                                                                                                                                                                                                                                           04-JUN-2002; 2002WO-US017428
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                                                                                                                                                                             WO200299116-A2
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                                                                                                                                                                                                 313 AGKKYFIDEVARETTCSKESNEELTESCETKKIGQSLDCNAEVYVVPWEKKIYPTVNCQP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor related protein; GPCR related protein; NOV; cytostatic; cardiant; antiarteriosclerotic; annidiabetic; immunomodulator; anti-HIV; anorectic; antiathmatic; haemostatic; antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; diabetes; immune disorder; AIDS; obesity; asthma; haematopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; wasting disorder; chronic disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
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                                                                                                                             1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                        253 GKDFVQPPTKICVGCPRDIPTNSPELBETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                  61 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
                                                                                                 Gaps
sequence of a novel human G-protein NOV
                                                                                                 ;
                                                                        Length 644;
                                                                                                 Indels
                                                                     Score 660; DB 6;
Pred. No. 2.3e-65;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human GPCR related protein NOV12c.
                                                                                                                                                                                                                                                                                                                                        ABU99145 standard; protein; 644 AA.
  vaccines. This is the amino acid coupled receptor related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0295661P.
2001US-0296404P.
2001US-02982418P.
2001US-0298265P.
2001US-0299349P.
2001US-0299349P.
2001US-030083P.
2001US-0311972P.
2001US-0315071P.
2001US-0315071P.
                                                                     Query Match
Best Local Similarity 100.0%;
Matches 123; Conservative 0
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2001US-0341186P.
2002US-0361189P.
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                                                                                                                                                                                                                                         LGM 123
                                                                                                                                                                                                                                                                    LGM 375
                                            Sequence 644 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2001;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JJN-2001;
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29-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                  ABU99145;
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20-APR-2000; 2000WO-GB001571

WO200064945-A1

02-NOV-2000

99GB-00009133

22-APR-1999;

Mbrahamson M, Barrett AJ;

WPI; 2000-687316/67.

(BABR-) BABRAHAM INST

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Spytek KA,
         Gerlach VL, Gorman L, Guo X, Hie
, Malyankar UM, Millet I, Padigai
stelli L, Shimkets RA, Stone DJ,
                                                                                       Claim 1; Page 144-145; 332pp; English
     Baumgartner JC,
                            Zerhusen BD;
          Gangolli EA, Gerlach
Macdougall JR, Malya
Pena CEA, Rastelli L
Voss EZ, Zerhusen BD
                                        2003-140627/13
                                              N-PSDB; ACD03649.
                                                                            pharmacogenomics.
                                                                                                                                                                                                                                         Sequence 644 AA;
  Anderson DW,
Gangolli EA,
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253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312 09 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV Gaps . 0 Length 644; Indels Match 100.0%; Score 660; DB 6; Local Similarity 100.0%; Pred. No. 2.3e-65; es 123; Conservative 0; Mismatches 0; Query Match Matches Best 셤 à

313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP ||| LGM 375 LGM 123 61 121 373 a ò à

120

AAB37447 standard; protein; 122 AA. AAB37447; RESULT 15 AAB37447

(first entry) 21-FEB-2001

Human kininogen D3

Enzyme; legumain; endopeptidase; cystatin; human; kininogen.

Homo sapiens

The invention describes an isolated polypeptide (I) comprising any of 27 [18-96] residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95 *identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology of syndrome associated with the polypeptide. The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune disorders, AlDS, obesity, asthma, haematopoietic disorders, parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, owund healing and angiogenesis, in gene therapy, in generation of the therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein. New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or Boldog FL, Casman SJ, Edinger SR; nan L, Guo X, Hyalt T, Kekuda R, Li L; Millet I, Padigaru M, Patturajan M; ts RA, Stone DJ, Spytek KA, Vernet CAM;

Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of

Disclosure, Fig 4; 45pp; English

cystatin.

ô 9 The present invention relates to inhibition of the enzymatic activity of legumain or a legumain-related endopeptidase by cystatin. The inhibition involves an interaction between legumain and a papain-non-reactive site of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and performs a protein-processing function. The present sequence is human kininogen D3, which was used in the present invention. Kininogen is a type 3 cystatin 99 67 IDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLGM 123 PPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYF 1 PPTKICVGCPRDIPTNSPELBETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYF Gaps ; Length 122; Indels .. 0 Score 628; DB 3; Pred. No. 9.5e-63; 95.2%; Sco... 100.0%; Pred. No. >... '... 0; Mismatches Search completed: September 24, 2004, 14:08:37 Job time : 52.692 secs Query Match
Best Local Similarity 100.0
Matches 117; Conservative Sequence 122 AA; à 셤 ò

7

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 24, 2004, 14:04:32; Search time 8.364 Seconds (without alignments) 765.738 Million cell updates/sec Run on:

US-10-661-784-1 660 1 GKDFVQPPTKICVGCPRDIP......VVVPWEKKIYPTVNCQPLGM 123

Title:
Perfect score: (Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq lëngth: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES Description		HUMAN PO1042 homo	BOVIN P01046 bos	30VIN P01044	SOVIN P01047	77	KNG MOUSE 008677 mus musculu	P08934	P08932			О16096 hото	Q15828 homo	. P01035 bos t	019092	CYTC_SAISC 019093 saimiri sci	P14841	P21460	Q9qx79	OBUGE POMO	P08935 biti	P01034 homo	P09228 homo	oryo	P81061				P19313	P01037 homo	N P01036	NCKE Q98967 onco	KC05
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P22085 onchocerca	Q9d269 mus musculu	Q9h114 homo sapien	P32766 mus musculu	Q9h112 homo sapien	P29699 mus musculu	P81714 naja atra (P31726 zea mays (m	P28325 homo sapien	P24090 rattus norv	O60676 homo sapien	O88969 rattus norv
CYTX ONCVO	CS11_MOUSE	CSTL HUMAN	CST8 MOUSE	CS11 HUMAN	A2HS MOUSE	CYT NAJAT	CYT1 MAIZE	CYTD HUMAN	A2HS RAT	CST8 HUMAN	CST8_RAT
Н	Н	-	н	Н	-	Н	н	н	н	_	н
162	139	165	142	137	345	66	135	142	352	142	142
16.0	15.3	14.4	14.3	14.2	14.2	14.1	13.9	13.8	13.7	13.6	13.1
105.5	101	95	94.5	93.5	93.5	93	91.5	91	90.5	89.5	86.5
								42			

ALIGNMENTS

RESULT 1

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DOMAIN
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Seikagaku 56:808-808(1984).

RA CARBOHYDRATE-LINKAGE SITE ASN-294.

RA Chang H., ii X.-J., Martin D.B., Aebersold R.;

Andraif action and quantification of N-linked glycoproteins using reduction and quantification of N-linked glycoproteins using rate biotechnol. 21:660-666(2003).

RT Hodraide chemistry, stable isotope labeling and mass spectrometry.";

RA Biotechnol. 21:660-666(2003).

LE Biotechnol. 21:660-666(2003).

LE Biotechnol. 21:660-666(2003).

HWW-kininogen plays an important role in blood coagulation by helping to position optimally prekalikrein and factor XI next to the hologing and plays an important role in blood coagulation by helping to position of thromborytes; (4) the active peptide induced aggregation of thromborytes; (4) the active peptide bradykinin that is released from HWW-kininogen shows a variety of physiological effects; (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriures and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation of nociceptors (4E) it is a mediators of inflammation of nociceptors (4E) release of other mediators of inflammation of nociceptors (4E) release of coller mediators of inflammation (e.g. prostaglandins), (4F) it has a cardioprotective effect directly via bradykinin action, (5) LMW-kininogen is in contrast to HMW-kininogen not involved in blood clore, included in blood coagulation of thrombocytes; (6) LMW-included in blood coagulation of involved in blood coagulation of involved in blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P01042-2; Sequence=VSP_001261, VSP_001262;
-!- TISSUE SPECIFICITY: Plasma.
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
-!- SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                    clotting.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR PRODUCTS:
Event-Alternative splicing; Named isoforms=2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0007596; P:blood coagulation; NAS.
GO; GO:0030146; P:diuresis; NAS.
GO; GO:0006954; P:inflammatory response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P01042-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL, M11437, AABS9550.1, -
EMEL, M11438, AABS9550.1, -
EMEL, M11521, AABS9550.1, JOINED.
EMEL, M11522, AABS9550.1, JOINED.
EMEL, M11523, AABS9550.1, JOINED.
EMEL, M11524, AABS9550.1, JOINED.
EMEL, M11525, AABS9550.1, JOINED.
EMEL, M11526, AABS9550.1, JOINED.
EMEL, M11527, AABS9550.1, JOINED.
EMEL, M11527, AABS9550.1, JOINED.
EMEL, M11527, AABS9551.1, JOINED.
EMEL, M11521, AABS9551.1, JOINED.
EMEL, M11522, AABS9551.1, JOINED.
EMEL, M11523, AABS9551.1, JOINED.
EMEL, M11524, AABS9551.1, JOINED.
EMEL, M11525, AABS9551.1, JOINED.
EMEL, M11526, AABS9551.1, JOINED.
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PIR; A01280; KGHUH1.
SWISS-ZDPAGE; P01042; HUMAN.
GGENEW; HGNC: 6383; KNG.
MIM; 228960; -.
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PPKAGAEPASEREVS (in isoform LMW).
/FTIdevSP 001261.
Missing (in isoform LMW).
Missing (in isoform LMW).
TridevSP 001262.
T -> I (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 AGKKYFIDFVARETICSKESNEELTESCETKKLGGSLDCNAEVVVVPWEKKIYPTVNCQP
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                          Fram, PR0001; cystatin; 3.
PRINTS; PR00314; KININOGEN.
SMART; SM00043; CY; 3.
PROSITE; PS00287; CYSTAIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blod coagulation; Inflammatory response; Signal; Alternative splicing; Pyrrolidone carboxylic acid.
SIGNAL
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100.0%; Score 660; DB 1; Length 6
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 123; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                    KININOGEN.
KININOGEN HEAVY CHAIN.
BRADYKININ.
                                                                                                                                                                                        KININOGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
GO; GO:0030147; P.natriuresis; NAS.
GO; GO:0006939; Pismoch muscle contraction; NAS.
InterPro; IPRO00010; Cystatin.
InterPro; IPR002395; Kininogen.
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644 AA;
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CARBOHYD
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PEPTIDE
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DOMAIN
DOMAIN
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122 G 122
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P01044;
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                               DISULFID
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DISULFID
CONFLICT
SEQUENCE
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KNH1_BOVIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  MEDLINE=87137530; PubMed=3546295;

MEDLINE=87137530; PubMed=3546295;

MEDLINE=87137530; PubMed=3546295;

Miyata T., Miyata T., Hashimoto N., Kato H., Hayashida H.,

Miyata T., Iwanaga S.;

Misolo Collar weight kininogen. The amino acid sequence,

Discriptions of carbohydrate chains and disulfide bridges in the heavy

Colain portion...'

J. Biol. Chem. 262:2768-2779(1987).

Lim-kininogen inhibits the aggregation of thrombocytes; (2)

Lim-kininogen inhibits the aggregation of thrombocytes; (3) the

active peptide kallidin that is released from LMW-kininogen shows

a variety of physiological effects: (3A) influence in smooth

muscle contraction, (3B) induction of hypotension, (3C)

natriuresis and diuresis (Aidney).

SUBCELLULAR LOCATION: Extracellular.

C. SUBCELLULAR LOCATION: Extracellular.

C. SUBCELLULAR LOCATION: Extracellular.

Mame=LMW I;

Name=LMW I;

Mame=LMW I;

Mame LMW I;

Mame 
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DR PIR; A01283; XGB0LI.

DR Pfam; PF00031; Cystatin. 3.

DR SMART; SM00043; CYSTATIN; 2.

RW Thiol protease inhibitor; Bradykinin; Signal;

FT CHAIN 19 436 KININOGEN, LMW I.

THEAT 19 436 KININOGEN, LMW I.

THEAT 19 436 KININOGEN, LMW I.

THEAT 19 388 BRADYKININ.

THEAT 19 388 BRADYKININ.

THEAT CHAIN 389 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=8117859; PubMed=6572010;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
Nawa H., Kitamura S. Dovine Inver low molecular weight kininogen
precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
Kininogen, LMW I precursor (Thiol proteinase inhibitor) (Contains: Bradykinin).
Bos taurus (Bovine).
Bustryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
                 436 AA
                 STANDARD;
               BOVIN
               KNL1 BOV
P01046;
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DOMAIN
DOMAIN
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253 KDFVQPPTRLCAGCPKPIPVDSPDLEEPLSHSIAKLNAEHDGAFYFKIDTVKKATVQVVA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S., "A single gene for bovine high molecular weight and low molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 378-393.
MEDLINE=70180420; PubMed=4986212;
Kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Kininogen, HWW I precursor (Thiol proteinase inhibitor) [Contains: Bradykinin].
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bosinae; Bos.
1012_TaxID=9913;
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0
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48427 MW; FO1F7EB6814BCE6C CRC64;
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71.9%; Pred. No. 3.6e-38;
ive 14; Mismatches 20; Indels
PYRROLIDONE CARBOXYLIC AC
N.LINKED (GLCNAC. .).
O-LINKED (PARTIAL).
N.LINKED (GLCNAC. .) (C
N.LINKED (GLCNAC. .) (C
N.LINKED (GLCNAC. .))
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O-LINKED (PA
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N-LINKED (GI
INTERCHAIN.
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2. Biol. Chem. 262:2768-2779(1987).
[3]
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MEDLINE=84014106; PubMed=6571699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 71.9%
Hes 87; Conservative
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Nature 305:545-549(1983).
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436 AA;
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Name=HMW II;
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P01047;
DISULFID
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         VER DELINE -75170265; PubMed=1169237;

AM MEDLINE-75170265; PubMed=1169237;

Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

Han Y.N., Komiya M., Iwanaga S., Suzuki T.;

"Studies on the primary structure of bovine high-molecular-weight

"Trinogen. Amino acid sequence of a fragment ('histidine-rich

"Trinogen. 77:55-68(1975).

"Trinogen. 77:55-68(1975).

"Trinogen. 77:55-68(1975).

"Trinogen. Proprime action to by Horomotory and Factor XI next to factor XII; (3) Hww-kininogen inhibits the thrombin- and plasmin-

"Induced aggregation of thrombocytes; (4) the active peptide

"Trinogen aggregation of thrombocytes; (4) the active peptide

"Trinogen aggregation of thrombocytes; (4) the active peptide

"Trinogen shows a variety of physiological effects: (4) influence in smooth musche contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of a cardioprotective effect (directly via bradykinin action), indirectly via endothelium-derived relaxing factor action).

"Trinogen action of the physiologics and active splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Plasma.
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
-!- SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R EMBL; V01491; CAA24735.1; -.
R PIR; A01291; KGROUT.
R InterPro; IPR002395; Kininogen.
R InterPro; IPR002395; Kininogen.
R PRINTS; PR00334; Cystatin; 3.
R PRINTS; PR00334; KININOGEN.
R PRINTS; PR00341; CY3TIN; 3.
R PR05ITE; P800281; CY3TIN; 2.
R PR05ITE; P800281; CY3TIN; 2.
M Glycoprotein; Plasma; Pepeat; Vascdilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Infilammatory response; Signal; PR0BABLE.
R SIGNAL
I CHAIN
I CHAIN
I CHAIN
I CHAIN
I CHAIN
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N-LINKED (GLCNAC. .) (PARTIAL).
N-LINKED (GLCNAC. .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
O-LINKED (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KININOGEN, HWW I.
HEAVY CHAIN.
BRADYKININ.
LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                 IsoId=P01044-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                           Name=LMW I;
IsoId=P01046-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN
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204
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DOMAIN
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DOMAIN
MOD RES
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
PEPTIDE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                     313 GLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTVNCQPL 372
                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain portion.";

J. Biol. Chem. 262:2768-2779(1987).

J. Biol. Chem. 262:2768-2779(1987).

LIMW-kininogen inhibits the aggregation of thrombocytes; (3) the active peptide kallidin that is released from LMW-kininogen shows a variety of physiological effects: (3A) influence in smooth muscle contraction, (3B) induction of hypotension, (3C) nattiuresis and diuresis (kidney).

SUBCELINIAR LOCATION: Extracellular.
                                                                                                                                                                          2 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA
                                                                                                                                                                                                               62 GKKYPIDFVARETICSKESNEELTESCEIKKIGQSLDCNAEVYVVPWEKKIYPTVNCQPL
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: Plasma.
-!- PTM: Bradykinin is released from kininogen by plasma kallikrein.
-!- PTM: Bradykinin is released from kininogen by MSCELLANBOUS: LMW-kininogen is in contrast to HWW-kininogen not involved in blood clotting.
-!- SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 19-376...
MEDLINE-87137530; PubMed=3546295;
Sueyoshi T., Miyate T., Hashimoto N., Kato H., Hayashida H.,
Niyate T., Iwanaga S.;
Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
BEDILNE-S11785; PubMed-6572010;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
"Primary structures of bovine liver low molecular weight kininogen
                                                                                                                   ö
                                                    Length 621;
                                                                                                                   20; Indels
621 AA; 68890 MW; D16850BEFE3C55CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                    Query Match
72.3%; Score 477; DB 1;
Best Local Similarity 71.9%; Pred. No. 5.4e-38;
Matches 87; Conservative 14; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursors and their two mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=LMW II;
IsoId=P01047-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P01045-1; Sequence=External;
TISSUE SPECIFICITY: Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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MEDLINE=84014106; PubMed=6571699;
 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             310 GGLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTVNCQP 369
                                                                                                                                                                                                                                                                                                                                                 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
                                                                                                                                                                                                                                                                                                                      1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             KMHZ BOVIN STANDARD; PRT; 619 AA.

P01045;
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Kininogen, HWW II precursor (Thiol proteinase inhibitor) [Contains: Bradykinins]
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Bocora; Bovoidea;
                                                                            Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                        68.2%; Score 450; DB 1; Length 434;
68.9%; Pred. No. 1.4e-35;
ive 14; Mismatches 22; Indels 2;
                                                                                                                                                                               (OR 169).
(PARTIAL).
                                                                                                                                   CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .) (OR 169)
N-LINKED (GLCNAC. . .) (PARTIAL)
N-LINKED (GLCNAC. . .) (PARTIAL)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                            48148 MW; 73A7079DE3E03430 CRC64;
                                                                                                         KININOGEN, LMW II.
HEAVY CHAIN.
BRADYKININ.
                                                                                                                                LIGHT CHAIN.
                                                                                                                                                                                                            INTERCHAIN
                                  PIR, A01284; KGBOL2.
HSSP, P01038; 1A90.
InterPro, IPRO0010, Cystatin.
Pfam; PF00031; cystatin; 3.
SWART; SM00043; CY; 3.
PROSITE; PS00287; CYSTAIN; 2.
                            EMBL; V00427; CAA23710.1;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                           3336
3386
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356
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                                                                                                                                                                                                                                                                           434 AA;
                                                                                                                                                                                                                                                                                                Local Similarity
les 84; Conserv
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SEQUENCE FROM N.A.
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PEPTIDE
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The stants N. Takagashi Y. Pirmico S. Tanaka T., Nawa H., Nakanishi S., Faramara N. Takagashi Y. Pirmico S. Tanaka T., Nawa H., Nakanishi S., Sarahi S. Sara
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61 AGKKYPIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GGLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVPWEEKVYPTVNCQP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKDFVQPPTKICVGCPRDIPTNSPELEFILTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                        LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .) (OR 169).
N-LINKED (GLCNAC. . .) (OR 169).
N-LINKED (GLCNAC. . .) (PARTIAL).
N-LINKED (GLCNAC. . .).
                                                                tepeat; Vasodilator; Alternative splicing;
br; Bradykinin; Blood coagulation; Signal;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                 68.2%; Score 450; DB 1; Length 619;
68.9%; Pred. No. 2e-35;
live 14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                             198 T -> P.
101 L -> V.
164 H -> K.
68710 MW, F04320A8EBUEEUDA CRC64;
                                                                                                           KININOGEN, HMW II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NG MOUSE STANDARD; PRT; 661 AA. 008677; 008676; Q91XK5; 16-OCT-2011 (Rel. 40, Created) 15-OCT-2011 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Kininogen precursor [Contains: Bradykinin].
                                                                                                                       HEAVY CHAIN.
                                                                                                                                                                                                                                                                             INTERCHAIN.
                                                    PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodila
Thiol protease inhibitor; Bradykinin;
InterPro; IPR000010; Cystatin.
InterPro; IPR002395; Kininogen.
Pfam; PF00031; Cystatin; 3.
PRINTS; PR00334; KININOGEN.
SMART; SM00043; CY; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.9
Matches 84; Conservative
                                                                                      Inflammatory response;
SIGNAL 1 18
                                                                                                                                                                                                                                                                                                                                                                                                             619 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LG 122
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                                                                                                                                                      DOMAIN
DOMAIN
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MOD_RES
CARBOHYD
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VARIANT
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PEPTIDE
CHAIN
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                                                                                                                                                                                                                                                                   CARBOHYD
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SEQUENCE FROM N.A. (ISOFORMS HWW AND LMW). STRAIN=CS7BL/6 X CBA; TISSUE=Liver; MEDLINE=97342556; PubMed=9199253;

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EQUINER FROM N.A. (1907bW Law).

REQUIRES 2088057; Pubmed=12477932;

REDINIES=2188057; Pubmed=12477932;

RETAISSABLE FROM: Feingold E.A. Grouse L.H., Derge J.G., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin GM., Hong L.,

RA Explecton M., Soares M.B., Donaldow N.F., Carvinci P., Prange C.,

RA Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Ana S.S., Morley K.C., Hale S., Garrino P., Prange C.,

RA Ana S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Halton D.K., Walzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Allalon D.K., Walzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Allalon D.K., Walzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hakeabey R.W., Touchman J.W., Goffmut J., Wyers R.M.,

RA Hakeabey R.W., Touchman J.W., Goffmut J., Myers R.M.,

RA Antiguez A.C., Grimwood J., Schmut J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmut J., Myers R.M.,

RA Hakeabey R.W., Narywinski M.I., Skalska U., Smailus D.E.,

RA Honan and mouse copy, Schmut J.B., More than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation of thromosover langed and factor XI mext to

C Fector XII. (3) HWW-kininogens are inhibitors of thiol proteases; (2)

Hardykinin that is released from HWW-kininogen shows a variety of

C C C Charaction, (4B) induction of hypotension, (4C) natriures and

C C C Charaction, (4B) induction of hypotension, (4C) natriures

C C C Charaction, (4B) induction of hypotension, (4C) natriures

C C C Charaction, (4B) induction of hypotension, (4C) natriure mediator of inflammation and eases (4B1) increase in vascular

C C C C C C C C C C C C C C C C C 
                                                                                                                                                                                                                                                                           REAUTONICE FROM N.A. (ISOFORM LAW).

SEQUENCE FROM N.A. (ISOFORM LAW).

SCTRAIN=C57BL/6J; TISSUE=Placenta;

RADILINE=2534683; PubMed=12466851;

RADILINE=2534683; PubMed=12466851;

RADILINE=2534683; PubMed=12466851;

RADILINE=2534683; PubMed=12466851;

RADILINE=2534683; PubMed=12466851;

RADILINE, Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Radadarelli R., Hill D.P., Bult C., Humen D.A., Ouackenbush J., Dalla B., Dragani T.A., Matsuda H., Batalov S., Beisel K.W.,

RADIL B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RADIL B., Dragani T.A., Fletcher C.F., Forrest A., Gough J., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RADIL B., Navagani T.A., Lee Y., Lenhard B., Lyons P.A.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RADIL R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RADICH D.K., Maltais L., Marchionni L., McKenzie L., Miki H.,

RADILI R., Pontius J.U., Oi D., Remachandran S.,

RADILIA R., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Tasadale R.D., Tomit M.,

RADILIA R., Maner L., Wahlestedt C.A., Watanabe Y., Wells C.,

Williang L.G., Wynshaw-Boris A., Vanagisawa M., Yang I., Yang I.,

RADILA R., Ravai T., Konno H., Nakawa T., Tokh M., Kagawa I.,

RADILA R., Rabizume W., Incernic R., Ishii Y., Itoh M., Kagawa I.,

RADILA A., Sakai K., Sasaki D., Shinagawa A.,

RADILA A., Sakai K., Sasaki D., Shinaga R., Shinagawa A.,

RADILA R., Maltysis of the mouse transcriptome based on functional annotation of Struck R. Radila R. Taken R.
Takano M., Kondo J., Yayama K., Otani M., Sano K., Okamoto H.; "Molecular cloning of cDRAs for mouse low-molecular-weight and high-molecular-weight prekininogens."; Biochim. Biophys. Acta 1352:222-230(1997).
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61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCQP

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BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
VSPPYIAREQUERRALETEQUETHGHOWLHERQ.-> RLLRACETERGUETHGHOWLHERQ.-> RCEYMORTHGHOWLHERQ.-> RCEYMORTHGHOWLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00031; cystatin; 3.

PRINIS; PR00334; KININOGEN.
SMART; SM00043; CY; 3.

PROSITE; PS00287; CYSTATIN; 1.

Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
Bradykinin; Blood coagulation; Inflammatory response; Signal;
Alternative splicing.
a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action); (5) LMM-kininogen inhibits the aggregation of thrombocytes; (6) LMM-kininogen is in contrast to RMM-kininogen not involved in blood clotting (By similarity).

SUBCELLULAR LOCATION; Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                  IsoId=008677-2; Sequence=VSP_001263, VSP_001264;
TISSUE SPECIFICITY: Plasma.
PTM: BradyKinin is released from kininogen by plasma kallikrein.
SIMILARITY: Contains 3 cystatin-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VSP_001263.
Missing (in isoform LMW).
/FTIG=VSP_001264.
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BRADYKININ.
KININGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH.
                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                   IsoId=008677-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, D84415; BAA19742.1; -.
EMBL, AK005547; BAB54115.1; -.
EMBL, BC018158, AAH18158.1; -.
MGD, MGI.1097705; Kng.
INCEPPC, IPR000010; Cystatin.
InterPro; IPR000395; Kininogen.
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RC SEQUENCE OF 1-41 FROM N.A.

RC STRAINWWistar; TISSUE-Liver;

RX MEDLINE-87137465; PubMed=3818598;

REDLINE-87137465; PubMed=3818598;

REDLINE-88187465; PubMed=3818598;

REDLINE-88187465; PubMed=3818598;

REDLINE-88187465; PubMed=3818598;

REDLINE-88187465; PubMed=381858;

REDLINE-88187465; PubMed=381868;

REDLINE-88187465; PubMed=3818688;

REDLINE-88187465; PubMed=3818688;

REDLINE-88187465; PubMed=3818688;

REDLINE-88187466;

REDLINE-88187466;

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REDLINE-88187466
312 AGTKYVIEFIARETKCSKESNTELAEDCEIKHIGQSLDCNANVYMRPWENKVVPTVKCQA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Buffalo;
MEDLINE=87250580; PubMed=2439509;
Fung W.-P., Schreiber G.;
Structure accure of the genes for major acute phase alpha 1-
protein (thiostatin) and kininogen in the rat.";
J. Biol. Chem. 262:9298-9308(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM LMW).
MEDLINE=86008264; PubMed=2413018;
MEDLINE=8405., Mitamura N., Nakanishi S.;
Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S., "Differing expression patterns and evolution of the rat kininogen
                                                                                                                                                                                                                                                                                      P08934; P08933;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
MARA-2004 (Rel. 43, Last annotation update)
Kininogen precursor [Contains: Bradykinin].
                                                                                                                                                                                                                                                                     639 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 260:12054-12059(1985)
                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87137443; PubMed=3029068;
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                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                            121 LGM 123
                                                                                                                                372 LDM 374
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Conservative

81;

Matches

Query Match Best Local Similarity

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Gaps

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65.2%; Score 430; DB 1; Length 661; 65.9%; Pred. No. 1.8e-33; Indels tive 11; Mismatches 31; Indels

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Gaps

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us-10-661-784-1.rsp

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Pred. No. 4.1e-33;
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65.08; F1
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                                        80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
           Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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RWT2 RAT
TO KWA2 RAT
P08932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHGHGWLHAKO -> RLLNS
ASTVTP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
Bradykinin; Blood coagulation; Inflammatory response; Signal;
Alternative splicing; Multigene family.
SIGNAL
                                                                                                                                                               Insold=P08934-2; Sequence=VSP_001265, VSP_001266;
--- TISSUE SPECIFICITY: Plasma.
--- PTM: Bradykinin is released from kininogen by plasma kallikrein.
---- MISCELLANBOUS: Rats express four types of kininogens: the classical HWW/LMW kininogens and two additional LMW-like kininogens: T-I and T-II.
---- SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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CEYKGRLLKAGAGPAPERQAEASTVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FIId=VSP 001265.
Missing (in isoform LMW).
PTId=VSP 001266.
E -> K (IM REF. 2).
D3172DF94FP56AF5 CRC64;
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BRADYKININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KININOGEN LIGHT CHAIN.
                    clotting.
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Name=HMW;
Name=HMW;
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH.
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                                                                                                                              IsoId=P08934-1; Sequence=Displayed;
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EMBL; M11884; AAA41467.1; -.
EMBL; M14369; AAA41484.1; -.
EMBL; M14369; AAA41485.1; ALT_SEQ.
EMBL; M16455; AAA41482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BMBMJ, A25486, A25486.
PIR; A25486, A22486.
PIR; A28055; A28055.
InterPro; IPR003105, Cytatin.
InterPro; IPR002395; Kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 E
70933 MW;
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PRINTS; PR00334; KININOGEN.
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639 AA;
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                                                                                     312
                                                                                                                                                                          61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
                                                                                                                                                                                                                         9
                                                    Biol. Chem. 260:12054-12059(1985).
FYOYTON: Kininogens are plasma glycoproteins with a number of functions: (1) as precursor of the active peptide bradykinin they effect smooth muscle contraction, induction of hypotension and effect smooth muscle contraction, induction of hypotension and increase of vascular permeability. (2) They play a role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII. (3) They are inhibitor of thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANDOUS: Rats express four types of kininogens: the classical HMW and LMW kininogens produced by alternative splicing of the same gene, and two additional LMW-like kininogens: T-I and
1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Extracellular.

TISSUE SPECIFICITY: Plasma.

INDUCTION: In.response to an inflammatory stimulant. T-kininogen I synthesis is induced and the plasma concentration of T-kininogen I is raised.

PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IN IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=86608264; PubMed=2413018;
Puruto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
11-MAR-2004 (Rel. 43, Last annotation update)
T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiostatin) [Contains: T-kinin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 3 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 AA.
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us-10-661-784-1.rsp

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260:12065-12071(1985)
                                                                                                                                                                                                                                                                                                                                                                                                      IS NOT RELE
KALLIKREIN.
 Chem.
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DOMAIN
DISULFID
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CHAIN
PEPTIDE
CHAIN
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  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYPKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Furtice-Kato S., Matsumoto A., Kitamura N., Nakanishi S., "Pritice-Kato S., Matsumoto A., Kitamura D., Nakanishi S., "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YANTI_RAT STANDARD; PRT; 430 AA.
901048; P04081;
01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 09, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
T-kininogen I precursor (Major acute phase protein) (Alpha-1-MAP)
(Thiosetatin) [Contains: T-kinin].
                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDLINE=86008266, PubMed=2413019;
Anderson K.P., Heath B.C.;
"The relationship between rat major acute phase protein and thinnogens.";
                                                                                                                                                                                                                                                                                                                                                                           62.0%; Score 409; DB 1; Length 430; 61.8%; Pred. No. 1.1e-31; ive 15; Mismatches 32; Indels
                                                                                            CYSTATIN-LIKE 1.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY
                             inhibitor; Bradykinin; Acute phase; Signal
                                                                                                                                                                                                                                                                                                                                                   43EDF02D1BF55076 CRC64;
                Vasodilator; Multigene
                                                         T-II.
                                                                                                                                                                                                                                                                                                                                      (GLCNAC
                                                                     HEAVY CHAIN.
T-KININ.
                                                       KININOGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 260:12054-12059(1985).
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    CYSTATIN; 2.
                                                                                                                                                                                                                                                                                                                                                   47524 MW;
                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 61.8
nes 76, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                             18
3335
3375
1135
404
1125
217
                                                                                                                                                                                                                        PROSITE; PS00287; CYST
Glycoprotein; Plasma;
                                                                                                                                                                                                                                                                                                                                    326
430 AA;
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                                                       protease
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DISULFID
DISULFID
CARBOHYD
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CARBOHYD
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                                                       CHAIN
CHAIN
PEPTIDE
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KNT1 RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-87250580; PubMed-2439509; PubMed-2439509; Pung W.-P., Schreiber G.; Pung W.-P., Pung W.-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANBOUGS: Rats express four types of kininogens: the classical HMW and LMW kininogens produced by alternative splicing of the same gene, and two additional LMW-like kininogens: T-I and
SEQUENCE OF 7-430 FROM N.A. MEDITE 527561; Whole 12.7561; Whole 2577891; Whole 2577891; Whole 2577891; Whole 2577891; Whole 27.; Roch 12.; Roch 12.; Roch 12.; Roch 13.; Roch 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-Kininogen I is raised.
PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT
IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: Plasma.
INDUCTION: In response to an inflammatory stimulant. T-kininogen
II synthesis is induced and the plasma concentration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 3 cystatin-like domains.

CAUTION: In addition to the conflicts described in the feature table, Ref.2 sequence differs from that shown in positions 257, 262, 269, 295, 314, 315, 331, 332 and 389. In all those positions the alternate amino acid is the one present in T-II
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Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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EMBL; M11661; AAA41570.1; -.
EMBL; M16454; AAA41568.1; -.
EMBL; X02299; CAA26162.1; ALT_SEQ.
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InterPro; IPR000010; Cystatin.
Pfam; PF00031; cystatin; 3.
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PROSITE; PS00287; CYSTATIN; 2.
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PIR, A23897, A23897.
PIR, A27115, A27115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 KDLI---SSVKPGFPKTIETNNPGVLKAARHSVEKFNNCTNDIFLFKESHVSKALVQVVK 83
    Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;
"Leukocystatin, a new class II cystatin expressed selectively by
hematopoietic cells.",
J. Biol. Chem. 273:16400-16408 (1998)
J. Biol. Chem. 273:16400-16408 (1998)
J. FUNCTION: Inhibits papain and cathepsin L but with affinities
lower than other cystatins. May play a role in immune regulation
through inhibition of a unique target in the hematopoietic system.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVFKARVQVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GKKYFIDFVARETICSKESNEELIESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
(Leukocystatin) (Cystatin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 175; DB 1; Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYSTATIN F.
REACTIVE SITE.
SECONDARY AREA OF CONTACT.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B5837334C1B4A89C CRC64;
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PROBLE INDIBIOR; GlyCOProtein; Signal.
1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.5%; Score 1...
34.4%; Pred. No. 6.8e-1
--ive 23; Mismatches
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EMBL; P01034; 1036.
MGD; MG1:1298217; Cst7.
InterPro; IPR000010; Cystatin.
Pfam; P070031; Cystatin; SMART; SM00043; CY; 1.
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076096; Q9UED4;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seque
10-OCT-2003 (Rel. 42, Last annot
Cystatin F precursor (Leukocysta
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36 80
80 1
98 1
123 1
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SIGNAL 1
CHAIN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO 144
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SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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CYTF HUMAN
        임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDDLFELLPRYCRGCPREIPVDSPELKEALGHSIAQLNAQHNHIFYFKIDTVKKATSQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7) (Cystatin-like
                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] -
SEQUENCE FROM N.A.
MEDLINE=98298157; PubMed=9632704;
Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.8%; Score 401; DB 1; Length 430; 61.8%; Pred. No. 6.3e-31; ive 14; Mismatches 33; Indels
BY SIMILARITY.
BY SIM
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28-FEB-2003 (Rel. 41, Last amotation update)
28-Statin Precursor (Leukocystatin) (Cystatin metastasis-associated protein) (CMAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CST7.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47715 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (
15-DEC-1998 (
28-FEB-2003 (
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089098;
                                                                                                  DISULFID
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CONFLICT
CONFLICT
CONFLICT
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CONFLICT
SEQUENCE
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                                                                                 DISULFID
                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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NEDLINE-21638749; PubMed=11780052;

NEDLINE-21638749; PubMed=11780052;

NEDLINE-21638749; PubMed=11780052;

A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

Bassley O.P., Bird C.P., Batler A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.B., Coller R.B., Connor R.B., Corby N.R.,

Clegg S., Colley V.B., Coller R.B., Connor R.B., Corby N.R.,

Clegg S., Colley V.B., Coller R.B., Dhami P.D., Dunn M.,

Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,

Coulson A.G., Frankland J.A., Fraser A., French L., Garner P.,

A Hammond S., Harley J.L., Heath P.D., Howlen P.J.,

Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson C.M., Johnson D.,

Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Anther S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

Anthe S.A., Mistry D., Moore M.J.F., Pearce T.A.V., Peck A.I.,

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Tracey A., Tromans A.C., Vaudin M., Walls M., Wallis J.M., Williep D.L., Willings D.,

Whithehead S.L., Whittehead S.L., Williep D.L., Williams L., Williams S.A.,

Williming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung;

XX MIDLINE=22388251; PubMed=12477932;

XX Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

XA Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

An Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

An Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                       SEQUENCE FROM N.A.
MEDLINE=99298157; PubMed=9632704;
MEDLINE=99298157; PubMed=9632704;
Malfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;
"Leukocystetin, a new class II cystatin expressed selectively by
hematopoietic cells.";
J. Biol. Chem. 273:16400-16408(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20399571; PubMed=10945474;
Morita M., Hara Y., Tamai Y., Arakawa H., Nishimura S.;
"Genomic construct and mapping of the gene for CMAP
(Leukocystatin/Cystatin F, CSI7) and identification of a proximal
novel gene, BSCv (C200rf3).";
Genomics 67:87-91(2000).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Moshiuchi N.; Morite M., Arakawa H., Yoshiuchi N.; "Human homologue of murine CMAP."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
proteinase inhibitor.";
J. Biol. Chem. 273:24797-24804(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEIGRITCKKNQHLRL-DDCDFQTNHTLKQTLSCYSSVWVVPWLQHFEVPVLRC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 CYSTAIN F.
37 REACTIVE SITE.
85 SECONDARY AREA OF CONTACT.
10 BY SIMILARITY.
62 N-LINKED (GECNAC. . ) (POTENTIAL).
115 N-LINKED (GECNAC. . ) (POTENTIAL).
16454 MW, B2BCC4776857CBOF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.1%; Score 165.5; DB 1; Length 145; 32.5%; Pred. No. 5.5e-09; ive 22; Mismatches 50; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0004869; F:cysteine protease inhibitor activity; TAS. GO; GO:0006955; P:immune response; TAS. IPRO00010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00287; CYSTATIN; FALSE NEG.
Thiol protease inhibitor; Glycoprotein; Signal.
SIGNAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTM HUMAN STANDARD, PRT; 149 AA. 015828, 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) CST6.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF036342; AAC35747.1; --
EMBL; AF031824; AAC39788.1; --
EMBL; AB015225; BAA34941.1; ALT_INIT.
EMBL; AL035661; CAB75498.1; --
EMBL; AL035661; CAB75498.1; --
EMBL; AL03561; CAB75498.1; --
EMBL; AL0364; CAB75498.1; --
EMBL; AL0364; LG964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00031; cystatin; 1.
SMART; SM00043; CY; 1.
PROSITE; PS00287; CYSTATIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:2479; CST7.
MIM; 603253; -.
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81
124
124
124
115
115
145 AA;
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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CYTM HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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inhibitor activity; morphogenesis; TAS.

ä 67 8

Gaps

7;

Indels

DB 1; Length 149;

Score 138.5; DB 1 Pred. No. 2.1e-06; 22; Mismatches

21.0%; 31.5%;

.) (POTENTIAL)

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8 PIKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 109
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                                                                                                                                                                                                                                                       26 PROBABLE.
149 CYSTATIN M.
27 SECONDARY AREA OF CONTACT.
28 SECONDARY AREA OF CONTACT.
213 BY SIMILARITY.
214 BY SIMILARITY.
215 BY SIMILARITY.
217 N-LINKED (GLCNAC. . .) (POTE
                                                                             Pfam; PR00010; Cystatin.

Pfam; PF00031; cystatin, 1.

SMART; SW00043; CY; 1.

PROSITE; PS00287; CYSTATIN; 1.

PROI protease inhibitor; Signal; Glycoprotein.
SIGNAL 1.
                        GO; GO:0004869; F:cysteine protease GO; GO:0007345; P:embryogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                             36
80
98
126
137
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 37-148
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MIM; 601891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTC BOVIN
                                                                                                                                                                                                                                                                                                                          ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTC_BOVIN
                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Protestate:

X Tatasberg Rouge In The Property of Tatasberg Strong No. 1.

X Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

X Rausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Wang J., Heng L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Willialon D.K., Mundy D.M., Schergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Richards S.W., Moray D.M., Scheutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ruman and mouse CONA sequences.";

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITES=1146880; PubMed=11148457; Zeeuwen P.L., Van Vlijmen-Willems I.M., Jansen B.J., Sotiropoulou G., Curfs J.H., Mens J.F., Jansen J.J., Van Ruissen F., Schalkwijk J.; Zeeuwen P.L., Van Vlijmen-Willems I.M., Jansen B.J., Schalkwijk J.; Zeeuwen P.L., Van Starsen F., Schalkwijk J.; Cystatin M.E expression is restricted to differentiated epidermal keratinocytes and sweat glands: a new skin-specific proteinase inhibitor that is a target for cross-linking by transglutaminase."; J. Invest. Dermatol. 116:693-701(2001).

-I. SUBCELDUARE LOCATION: Secreted.
-I. SUBCELDUARE LOCATION: Secreted.
-I. SUBCELDUARE LOCATION: Secreted.
-I. TISSUE SUBARETICHY: Restricted to the stratum granulosum of normal skin, the stratum granulosum/spinosum of psoriatic skin, and the secretory coils of eccrine sweat glands. Low expression levels are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found in the nasal cavity.
PTM: Substrate for transglutaminases. Acts as an acyl acceptor but not as an acyl donor.
                                                                                           Sotiropoulou G., Anisowicz A., Sager R.;
"Identification, cloning, and characterization of cystatin M, a novel
"Cysteine proteinase inhibitor, down-regulated in breast cancer.";
J. Biol. Chem. 272:903-910(1997).
                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
SEQUENCE M.A., Grubb A., Su J.,
Yu G.L., Li Y., Parmelee D., Xing L., Coleman T.A., Gentz S.,
Thotakura R., Nguyen N., Hesselberg M., Gentz R.;
Thotakura R., Nguyen N., Hesselberg M., Gentz R.;
Thotakura R., Nguyen P., Hesselberg M., Gentz R.;
Thotakura R., Nguyen P., Hesselberg M., Gentz R.;
Thotakura I. Nguyen N., Hesselberg M., Gentz R.;
Structural resemblance to family 2 cystatins.";
J. Biol. Chem. 272:10853-10858(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: Belongs to the cystatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND TISSUE SPECIFICITY.
                                                                   MEDLINE=97150844; PubMed=8995380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U62800; AAB06566.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION,
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                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE B23.100; PubMed=3891407;
Mirado M., Tsunasawa S., Sakiyama F., Niinobe M., Fujii S.;
Hirado M., Tsunasawa S., Sakiyama F., Niinobe M., Fujii S.;
Complete amino addi sequence of bovine colostrum low-Mr cysteine
profesinase inhibitor.";
FEBS Lett. 186.41-45(1985).
-i FUNCTION: This is a thiol proteinase inhibitor.
-i FUNCTION: This is a thiol
-i MASS SPECTROMETRY. WHA13420; METHOD=MALDI.
-i SIMILARITY: Belongs to the cystatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SEQUENCE OF 66-83, AND CHARACTERIZATION.
TISSUB-Ecrebrospinal filld, and Choroid plexus;
MEDLINE-98094199; Pubmed-9434110;
Olsson S.-L., Ek B., Wilm M., Broberg S., Rask L., Bjoerk I.;
Molecular cloning and N-terminal analysis of bovine cystatin C diachtification of a full-length N-terminal region.";
Biochim. Biophys. Acta 1343:203-210(1997).
                                                                                            21-JUL-1986 (Rel. 01, Created)
1-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cystatin C precursor (Colostrum thiol proteinase inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y10811; CAA71771.1; -. HSSP; P01034; 1G96.
STANDARD;
                                                DEPTH ```

EMBL; BC031334; AAH31334.1; -. HSSP; P01038; 1CEW. Genew; HGNC:2478; CST6.

us-10-661-784-1.rsp

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 S.
 48 NEEGVQEALSFAVSEFNKRSNDAYQSRVVRVVRARKQVVSGMNYFLDVELGRITCIK--S 105
 -i- FUNCTION: As an inhibitor of cysteine proteinases, this protein is thought to serve an important physiological role as a local regulator of this enzyme activity.
-i- SIMILARITY: Belongs to the cystatin family.
 22 NSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN
 ch 20.6%; Score 136; DB 1; Length 148; l Similarity 30.6%; Pred. No. 3.7e-06; 34; Conservative 22; Mismatches 31; Indels 24; Gaps
 PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
 82 BELTESC-----CTKKLGQSLDCNAEVYVVPWEKKIYPTVN----CQ 119
 Thiol protease inhibitor; Signal, Pyrrolidone carboxylic acid. SIGNAL 1 30 PROBABLE.
 MEDLINE=97054523; PubMed=8898820;
Wei L.H., Walker L.C., Levy E.;
Cystatin C. Icelandic-like mutation in an animal model of
cerebrovascular beta-amyloidosis.";
Stroke 27:2080-2085(1996).
 REACTIVE SITE.
SECONDARY AREA OF CONTACT
BY SIMILARITY.
 146 BY SIMILARITY.
16265 MW; BE740FE37CFB9F0E CRC64;
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 146 AA
 PRT;
 BY
 Macaca mulatta (Rhesus macaque).
 IPR000010; Cystatin.
 CY; 1.
 Pfam; PF00031; cystatin; 1.
SMART; SM00043; CY; 1.
PROSITE; PS00287; CYSTATIN;
 STANDARD;
 31
40
112
146
 Cystatin C precursor.
 102
126
148 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9544;
 15-JUL-1998
28-FEB-2003
 MACMU
 InterPro;
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 DISULFID
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 .
ن
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 88
 13 VGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVAR 72
 95
 this protein is
 6 QPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKY
 36 IGGPMDASVEEEGVRRALDFAVSEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVEMG
 Saimiri sciureus (Common squirrel monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Platyrrhini; Cebidae, Cebinae, Saimiri.
NCBI_TaxID=9521;
 Gaps
 -1- FUNCTION: As an inhibitor of cysteine proteinases, this prolitiought to serve an important physiological role as a local regulator of this enzyme activity.
-1- SIMILARITY: Belongs to the cystatin family.
 7;
 ..
S
 Length 146;
 Length 146;
 66 FIDFVARETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE 109
 SEQUENCE FROM N.A.
MEDLINE=97054523; PubMed=8898820;
Wei L.H., Walker L.C., Levy E.;
"Cystelin C. Icelandic-like mutation in an animal model of
 Indels
 REACTIVE SITE.
SECONDARY AREA OF CONTACT.
BY SIMILARITY.
BY SIMILARITY.
 F0B3BB774A29DF26 CRC64;
 08196353C0306AA3 CRC64;
 73 ETTCSKESNEELTESC --- ETKKLGQSLDCNAEVYVVPWE 109
 48;
 20.1%; Score 132.5; DB 1; 29.0%; Pred. No. 7.8e-06; ive 21; Mismatches 45;
 DB 1;
 20.2%; Score 133.5; DB 1
29.0%; Pred. No. 6.3e-06;
ive 21; Mismatches 48
 EMEL: U52028; AAB64051.1; -.
HSSP; P01034; 1G96.
InterPro; IPR000010; Cystatin.
Pfam; PF00031; CYStatin; 1.
SWART; SM00043; CY; 1.
PROSTTE; P500287; CYSTATIN; 1.
Thiol protease inhibitor; Amyloid; Signal.
SIGNAL
7 AMYLOID STATIN C.
7 AMYLOID STATIN C.
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 146 AA
BY SIMILARITY
 cerebrovascular beta-amyloidosis.";
Stroke 27:2080-2085(1996).
 143 B
15946 MW;
 143 E
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 Ouery Match
Best Local Similarity 29.0%;
Marches 31; Conservative
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Les 29; Conservative
 STANDARD;
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 Cystatin C precursor.
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Search completed: September 24, 2004, 14:09:12 Job time : 23.364 secs

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September 24, 2004, 14:05:18; Search time 35.424 Seconds (without alignments) 1095.549 Million cell updates/sec
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660
1 GKDFVQPPTKICVGCPRDIP......yvvPWEKKIYPTVNCQPLGM 123
 1017041
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Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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1: Sp_archea!:*

2: Sp_bacteria:*

3: Sp_fungi:*

4: Sp_human:*

5: Sp_inverebrate:*

6: Sp_mammal:*

7: Sp_inc:*

8: Sp_organelle:*

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2: Sp_organelle:*

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Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|   |        | Description     | Q7yrp6 sus scrofa | P70517 rattus norv | Q63581 rattus norv | Q9qw15 mus musculu | Q7z4j8 homo sapien | Q7zy91 xenopus lae | 07syh2 xenopus lae | Q801e5 xenopus lae | Q9epx9 mus musculu | Q800s8 brachydanio | Q801z5 cyprinus ca | Oscb17 mus musculu | Q9nh95 litomosoide | Q80y72 mus musculu | Q8k397 mus musculu | Ogdibi mus musculu |
|---|--------|-----------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|   |        | ΠD              | Q7YRP6            | P70517             | 063581             | Q9QWL5             | Q7Z4J8             | Q72Y91             | Q7SYH2             | Q801E5             | Q9EPX9             | Q800S8             | Q801Z5             | Q8CB17             | Q9NH95             | Q80Y72             | Q8K397             | 0901B1             |
|   |        | DB              | 9                 | 11                 | 11                 | 17                 | 4                  | 13                 | 13                 | 13                 | 11                 | 13                 | 13                 | 11                 | 'n                 | 11                 | 11                 | H                  |
|   |        | Match Length DB | 140               | 423                | 430                | 167                | 167                | 462                | 462                | 465                | 140                | 455                | 464                | 388                | 148                | 140                | 146                | 149                |
| æ | Query  | Match ]         | 61.2              | 6.09               | 60.5               | 26.5               | 25.1               | 23.1               | 23.1               | 23.1               | 19.6               | 18.6               | 17.9               | 17.5               | 17.2               | 17.1               | 16.8               | 16.8               |
|   |        | Score           | 404               | 402                | 399                | 175                | 165.5              | 152.5              | 152.5              | 152.5              | 129.5              | 122.5              | 118                | 115.5              | 113.5              | 113                | 111                | 111                |
|   | Result | No.             |                   | N                  | m                  | 4                  | ស                  | 9                  | 7                  | <b>0</b> 0         | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

| Q98sr4 acipenser s<br>Q98sr3 acipenser s<br>Q9tyy2 caenorhabdi<br>Q801z6 cyprinus ca<br>Q9ty65 onchocerca<br>Q9tm84 mus musculu | Q8vhcl rattus norv<br>O16159 brugia mala<br>Q9u9al onchocerca<br>P90698 brugia mala<br>Q8a65 sandersonia<br>Q8c0y2 sarcophaga | Q41825 zea mays (m O61973 ceanorhabdi O44396 haemonchus Q84396 haemonchus Q87503 ratus norv Q9fxn6 arabidopsis Q87xx7 arabidopsis Q21006 arabidopsis O2202 arabidopsis | P93627 zea mays (m Q41897 zea mays (m Q41897 zea mays (m Q9dapl mus musculu Q80zn5 mus musculu Q866w0 nippoetrong Q39270 brassica ca |
|---------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|
| Q98SR4<br>Q98SR3<br>Q9TYY2<br>Q801Z6<br>Q9TY65                                                                                  | Q8VHC1<br>Q8VHC1<br>Q9U9A1<br>P90698<br>Q8SA65<br>Q8T0Y2                                                                      | Q41825<br>O61973<br>O61973<br>Q61396<br>Q88XM6<br>Q17108<br>Q8K5A3<br>Q8FXM6<br>Q9FXM6<br>Q41906<br>O22202                                                             | P93627<br>Q41897<br>Q9DAP1<br>Q80ZN5<br>Q966W0<br>Q39270                                                                             |
| O O                                                                                                                             | 999999                                                                                                                        |                                                                                                                                                                        | O                                                                                                                                    |
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|                                                                                                                                 | 11<br>11<br>12<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13                                  | 144.<br>114.<br>113.<br>12.<br>13.<br>13.<br>14.<br>14.<br>14.<br>14.<br>14.<br>14.<br>14.<br>14.<br>14.<br>14                                                         | 13.4<br>13.3<br>13.0<br>12.0<br>12.0                                                                                                 |
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# ALIGNMENTS

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|------------------|--------------|---------|-------------|----------------------|--------------------|--------------------------------------------|------|--------|---------------------------------|---------------------------------|------------------|----|--------------------|-----------------------------------|-----------------------------|-----------------------------------------------------------------|--------------------------------------------|------------------------------------|-----------------------------|---------|-----|-------------------------|-------------|----------------|--------------------------------------------------------------|----------|-------------------------------------------|---|
|                  |              |         |             |                      |                    |                                            |      |        |                                 |                                 |                  |    |                    | ŭ.,                               |                             | Plasma                                                          |                                            |                                    |                             |         |     |                         |             | Gaps           | NSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN |          |                                           |   |
|                  |              |         |             |                      |                    |                                            |      |        | Euteleostomi;                   |                                 |                  |    |                    | Silva                             |                             | s and                                                           |                                            |                                    |                             |         |     |                         |             | 0;             | ARETTO                                                       | ARETTO   |                                           |   |
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|                  |              |         |             | <u>.</u>             | te)                |                                            |      |        |                                 |                                 |                  |    |                    | h M.D                             |                             | Kini                                                            |                                            | tabas                              |                             |         |     | CRC64                   | Lengt       |                | AGKKY                                                        | AGKKY    | 15 122                                    | _ |
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|                  | 140 AA.      |         |             | Last sequence update | annotation update) | ent).                                      |      |        | Chordata; Craniata; Vertebrata; | Cetartiodactyla; Suina; Suidae; |                  |    |                    | Ross J.A., Ashworth M.D., DeSilva |                             | "Porcine Endometrial and Conceptus Expression of Kininogens and | Kallikrein in Cyclic and Pregnant Gilts."; | to the EMBL/GenBank/DDBJ databases |                             |         |     | 177837836603F777 CRC64; | u           | 5; Mismatches  | DNVKK                                                        | GPVEK    | EELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPLG | _ |
|                  | PRT;         |         | Created)    | t segu               | annc               | Low molecular weight kininogen (Fragment). | ,    |        | raniat                          | cyla;                           |                  |    |                    | oss J.                            |                             | tus Ex                                                          | nt Gil                                     | L/GenE                             |                             |         |     | 177837                  | Score 404;  | Misma<br>Misma | PYFKI                                                        | VEYFKI   | VVVPWE                                    |   |
|                  | 24           |         |             |                      | , Last             | oden                                       | ,    |        | ta; C                           | iodac                           |                  |    |                    | C., R                             |                             | ouceb                                                           | regna                                      | e EMB                              |                             |         |     |                         |             | Ŋ              | AENNA                                                        | AENNA'   | CNAEV                                     | _ |
|                  | ARY;         |         |             |                      |                    | kinin                                      |      |        | Chorda                          | etart                           |                  |    |                    | Fernando S.C.,                    | Malayer J.R., Geisert R.D.; | and C                                                           | and P                                      | to th                              | EMBL; AY321363; AAP85260.1; | _       | 140 | 15650 MW;               | 61.2%;      | ive            | TITKLN                                                       | IAKLN    | disco                                     | _ |
|                  | PRELIMINARY; |         | (TrEMBLrel. | [TrEMBLre].          | (TrEMBLrel.        | eight                                      | 1    |        |                                 |                                 |                  |    | A.                 | Fernar                            | eisert                      | trial                                                           | yalia                                      | 2003)                              | AAP8                        |         | П   |                         | į           | Conservative   | ETLTH                                                        | EPLNHS   | CETKKI                                    |   |
|                  | PRE          |         | _           |                      |                    | llar w                                     |      | (Pig). | Eukaryota; Metazoa;             | Mammalia: Eutheria;             | NCBI TaxID=9823; |    | SECUENCE FROM N.A. | Α.                                | Я.                          | Indome                                                          | inc                                        | Submitted (JUN-2003)               | 1363;                       | Н       | 140 | 140 AA;                 |             | Con            | SPELE                                                        | SPDLE    | ELTES                                     | _ |
|                  | 96           | . 96    | 01-OCT-2003 | 01-OCT-2003          | 01-CCT-2003        | nolecu                                     |      | scrofa | ryota;                          | lia:                            | Taxid            | 1  | SNCE F             | Vonnahme K.A.,                    | /er J.                      | ine E                                                           | ikrein                                     | itted                              | , AY32                      | LER     | TER | SNCE                    | atch        | 79;            | 22 N                                                         | . д<br>Н | 82<br>EI                                  |   |
| LT 1.            | Q7YRP6       | Q7YRP6; | 01-0        | 01-0                 | 01-0               | Low                                        | KAG. | Sus    | Eukaı                           | Mamme                           | NCBI             | Ξ  | SEOU               | Vonne                             | Malay                       | "Porc                                                           | Kall                                       | Subm                               | EMBL                        | NON TER | NON | SEQUENCE                | Query Match | Matches        |                                                              |          |                                           |   |
| RESULT<br>O7YRP6 | ΩĤ           | AC      | μ           | Δ                    | μ                  | DE                                         | Ν̈́  | SO     | ပ္ပ                             | ပ္ပ                             | ŏ                | RN | RР                 | æ                                 | æ                           | RT                                                              | RT                                         | Z.                                 | DR                          | Н       | FT  | So                      | S 6         | MΣ             | ઠે                                                           | qq       | ò                                         |   |

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NCBI_TaxID=10116;
 121 LGM 123
 LDM 374
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 245 GDDLFELLPKNCRGCPREIPVDSPELKEALGHSIARLNAQHNHIFYFKIDTVKKATSQVV 304
 61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 305 AGVIYVIEFIARETNCSKQSKTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA 364
 MEDLINE=85127651; PubMed=2578992;

MEDLINE=85127651; PubMed=2578992;

MEDLINE=85127651; PubMed=2578992;

MEDLINE=85127651; PubMed=2578992;

MEDLINE=85127651; PubMed=2578992;

Major acute phase alpha1-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.";

FEBS Lett. 182:57-61[1955].

REBBL; K02814; AAA41569.1; -...

REBBL; K02814; AAA41569.1; -...

REBBL; K02814; AAA41569.1; -...

REBBL; K02814; AAA41569.1; -...

REBBL; K02814; PIRCO0010; Cystetine protease inhibitor activity; IEA.

RINE=FPC, IPROU031; Cystatin. 3.

REPROSITE; PS00287; CYSTATIN; 2.
 9
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
 Rat T-kininogen (T-KG).
Rattus norvegicus (Rat).
Ebkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 katuus norvegidus (kat).
Bukaryota, Metaeria, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 Cole T., Inglis A., Nagashima M., Schreiber G.; "Major acute-phase alpha(11-protein in the rat: Structure, molecular cloning, and regulation of mRNA levels."; Biochem. Biophys. Res. Commun. 126:719-724 (1985).
 0; Gaps
 Match 60.9%; Score 402; DB 11; Length 423; Local Similarity 61.8%; Pred. No. 3.1e-32; Los 76; Conservative 14; Mismatches 33; Indels (
 Cole T.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FCT-2003 (TrEMBLrel. 25, Last annotation update)
Major acute phase alpha-1 protein precursor (Fragment).
 423 AA; 46905 MW; F9E8BD3198547949 CRC64;
 Last sequence update)
Last annotation update)
 430 AA
 423 AA
 POTENTIAL. POTENTIAL.
 POTENTIAL
 Created)
 SEQUENCE FROM N.A.
MEDLINE=85149311; PubMed=2579644;
 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
 PRELIMINARY;
 PRELIMINARY;
 1
11
423
379
 Rattus norvegicus (Rat)
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 121 LGM 123
 365 LDM 367
 SEQUENCE
 Query Match
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 Q63581
Q63581;
 P70517
P70517;
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AC 06355
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DT 01-N
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 311
 61 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 371
 9
 STRAIN=CSTRL/6J TISSUE=Embryo;

NEDLINE=21085660; Pubmed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gasterland T., Gissi C., King B., Rochiwa H.,

Kuchi P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
 Gaps
 Mus musculus (Mouse).
Stakaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthezia; Rodentia; Sciurognathi; Muridae; Mus.
 ..
 PIR, S68035; S68035.

GO; GO: 0004669; F: cysteine protease inhibitor activity; IEA.
InterPro; IPR00010; Cystatin.
SMART; SM00041; CY; 3.
FROSITE; PS00287; CY: 3.
PROSITE; PS00287; CYSTATIN; 2.
SEQUENCE 430 AA; 47618 MW; 45508DEF4BDC978C CRC64;
 Length 430;
 / Match 60.5%; Score 399; DB 11; Length 4. Local Similarity 61.8%; Pred. No. 6.3e-32; hes 76; Conservative 13; Mismatches 34; Indels
 Anderson K.P., Croyle M.D., Lingrel J.B.; "Primary structure of a gene encoding rat T-kininogen."; Gene 81:119-128(1989).
 SEQUENCE FROM N.A. Moshiuchi N.; Morites M., Arakawa H., Yoshiuchi N.; Anovel Cystatin-like metastasis associated gene."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 Q9QWL5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
Murine CMAP (CYSTATIN F) (IBUKQCYSTATIN).
 167 AA
 EMBL; M29090 AAA42251.1; EMBL; M29080; AAA42251.1; JOINED. EMBL; M29081; AAA42251.1; JOINED. EMBL; M29081; AAA42251.1; JOINED. EMBL; M29085; AAA42251.1; JOINED. EMBL; M29086; AAA42251.1; JOINED. EMBL; M29087; AAA42251.1; JOINED. EMBL; M29089; AAA42251.1; JOINED. EMBL; M29089; AAA42251.1; JOINED. EMBL; M29089; AAA42251.1; JOINED. EMBL; M29089; AAA42251.1; JOINED. EMBL; S68034; S68034.
 MEDLINE=90034172; PubMed=2806908;
 PRELIMINARY;
 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
 NCBI TaxID=10090;
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Query Match
Best Local
 Q7SYH2
 RESULT 7
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 54 SRVKPGFPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 113
 62 GKKYPIDFVARETICSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVN 117
 68
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
"Functional annotation of a full-length mouse cDNA collection.";
BMBL, AB015224; BAA3494011;
BMBL, AR004420; BAB2329811;
BMBL, AR004420; BAB2329811;
 2 KDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVA
 9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID
 Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A., Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BTG09825, AAPB8827.1; -. SEQUENCE 167 AA, 18857 MW; E339025A5BD60177 CRC64;
 69 FVARETICSKESNEELIESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPIVNC 118
 114 VEIGRÍTÍCKKANQHLRÍ-DDCDFQTNHTÍKÓTLSCYSEVWVVÞWLQHFEVÞVLRC 166
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 .
0
 25.1%; Score 165.5; DB 4; Length 167; llarity 32.5%; Pred. No. 7.5e-09; Conservative 22; Mismatches 50; Indels 5
 26.5%; Score 175; DB 11; Length 167; ilarity 34.4%; Pred. No. 8.3e-10; Conservative 23; Mismatches 49; Indels
 HSDF, FULUST, LOCAT.
MGDF, MGI-1298217 CSt7.
GG; GO:G004865; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR00010; Cystatin.
Pfam, PP00031; cystatin; 1.
SEQUENCE 167 AA; 18847 MW; 61F776D8445095FE CRC64;
 Created)
Last sequence update)
Last annotation update)
 167 AA.
 PRT;
 01-0CT-2003 (TrEMBLrel, 25, 01-0CT-2003 (TrEMBLrel, 25, 01-0CT-2003 (TrEMBLrel, 25, Cystatin)
 PRELIMINARY;
 Query Match
Best Local Similarity
...aq 37; Conserva
 Query Match
Best Local Similarity
 Homo sapiens (Human)
 HSSP; P01034; 1G96.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 118 CO 119
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| 166 CQ 167
 42;
 Q724J8
 RESULT 5
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 8 PIKICVGCPRDIPINSPELEETLIHT----ITKLNAENNATFYFKIDNVKKARVQVVAGK 63
 8 PTKICVGCPRDIPTNSPELEETLTHT----ITKLNAENNATFYFKIDNVKKARVQVVAGK 63
 TISSUE=Ventral midgut;
Costa R.M.B., Mason J., Lee M., Amaya E., Zorn A.M.;
"Novel gene expression domains reveal early patterning of the Xenopus
 Gaps
 Gaps
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Cystatin domain fetuin-like protein.
Cystatin davis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Anura, Mesobatrachia, Pipidae,
 Eukaryota, Metazoa, Chordata, Craníata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
 5
 5;
 23.1%; Score 152.5; DB 13; Length 462; 38.8%; Pred. No. 5e-07; ive 13; Mismatches 34; Indels 5;
 DB 13; Length 462;
 Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO4391, AAH43891.1; -.
EMBL, BCO4391, AAH43891.1; -.
InterPro; IPR000010; Cystatin.
Pfam, PR0031, cystatin, 2.
SMART; SM00043; CY; 2.
SEQUENCE 462 AA; 53185 MW; D7BAD339961739FB CRC64;
 Query Match 23.1%; Score 152.5; DB 13; Length Best Local Similarity 38.8%; Pred. No. 5e-07; Matches 33; Conservative 13; Mismatches 34; Indels
 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY260732; AAP82289.1; -.
SEQUENCE 462 AA; 53186 MW; 796F92774CC27721 CRC64;
 (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
 201 SYFIOFTIKETDCMKTOENVVLSNC 225
 201 SYFIQFTIKETDCMKTQENVVLSNC 225
 64 KYFIDFVARETTCSKESNEELTESC 88
 64 KYFIDFVARETTCSKESNEELTESC 88
 01-JUN-2003 (TrEMBLrel. 24, Last seg
01-OCT-2003 (TrEMBLrel. 25, Last ann
Similar to fetuin B.
Xenopus laevis (African clawed frog)
 PRT;
PRT;
 33; Conservative
PRELIMINARY;
 PRELIMINARY;
 Xenopodinae; Xenopus
 Xenopodinae; Xenopus
 Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=8355;
 NCBI_TaxID=8355
 endoderm.";
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145 PGVILSTCP-DCPTANEEITPTITETAETLIAEYNKDSNNTRYFKIDHIERVRSGWVVGP 203
 STRAIN=BALB/c;
MEDLINE=21010502; PubMed=11144350;
Taupin P.J., Ray J., Fischer W.H., Suhr S.T., Hakansson K., Grubb A., Gage F.H.; Ray J., Eischer W.H., Suhr S.T., Hakansson K., Grubb A., Ray J., Ray J., Fischer W.H.; Suhr S.T., Hakansson K., Grubb A., Rage-2-Responsive neural stem cell proliferation requires CCg, a novel autocrine/paracrine cofactor.";
Neuron 28:385-397(2000).
 8 PTKICVGCPRDIPTNSPELEETLTHT----ITKLNAENNATFYFKIDNVKKARVQVVAGK
 "Cell-autonomous and signal-dependent expression of liver and
intestine marker genes in pluripotent precursor cells from Xenopus
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
 01-JUN'2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annocation update)
Hypothetical histidine-rich protein (Fragment).
Hypothetical histidine-rich protein (Fragment).
Encarcal African clawed frog).
Eukaryota, Metazca; Ghordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 Match 23.1%; Score 152.5; DB 13; Length 465; Local Similarity 38.8%; Pred. No. 5e-07; es 33; Conservative 13; Mismatches 34; Indels 5;
 Neuron 28:385-397(2000).
EMBL, ARSH1741; AAG40283.1; -.
EMBL, APSH1741; AAG40283.1; -.
HSSP, PO1034; LG95
GO: GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Cystein.
Pfam; PF00031; Cystein; 1.
SMART; SM00043; CY; 1.
PROSITE; PS00287; CYSTATIN; 1.
 Mech. Dev. 120:277-288(2003).

Mech. Dev. 188284; AA031610.1, .

GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Cystatin.
SMART; SM00031, cystatin, 2.

Mypothetical protein.
 Chen Y., Jurgens K., Hollemann T., Claussen M., Ramadori G.
Pieler T.,
 465 AA; 53528 MW; 0B403AB4F78BBFD4 CRC64;
 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 140 AA
465 AA
 204 SYFIQFTIKETDCMKTQENVVLSNC 228
 64 KYFIDFVARETTCSKESNEELTESC 88
 PRT;
PRT;
 MEDLINE=22480013; PubMed=12591597;
PRELIMINARY;
 PRELIMINARY;
 Cystatin C.
Mus musculus (Mouse).
 Xenopodinae, Xenopus.
NCBI_TaxID=8355;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Q801E5;
01-JUN-2003
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Matches 33
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 68
 72
 13 VGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVAR
 10 KICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQ-VVAGKKYFID
 Gaps
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 %0.0125,
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Fetuin long form
Cyprinus carpio (Common carp).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii; Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
 L Submitted (JAM-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY217758; ARCHG183.1; Cardited (JAM-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY217758; Cardital 1.1; Cardital 1.1; Cardital 2.1; Cardital
 69 FVARETICSKESNEELTES------CETKKLG-QSLDCNAEVY 104
 19.6%; Score 129.5; DB 11; Length 140; ilarity 30.0%; Pred. No. 2.6e-05; Conservative 21; Mismatches 44; Indels 5;
 18.6%; Score 122.5; DB 13; Length 455; 26.4%; Pred. No. 0.00052; ive 22; Mismatches 44; Indels 15;
16 16 A -> G.
84 84 L -> F.
140 AA; 15517 MW; 3A563406DD58D785 CRC64;
 90 RITCIK-SQINLID-CPFHDQPHLMRKALCSFQIYSVPWK 127
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 73 ETTCSKESNEELTESC---ETKKLGQSLDCNAEVYVVPWE
 Ą.
 455 AA
 PRT;
 29; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Best Local Similarity
 Similarity
 Cyprinidae; Danio.
NCBI_TaxID=7955;
 SEQUENCE FROM N.A. TISSUE=Liver;
 VARIANT
SEQUENCE
 Query Match
 Query Match
 Local
 Jia F.;
 VARIANT
 080088;
 980089
 Q801Z5
 RESULT 11
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AC 08012
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49 EIQEMLPSILIKVNQQSNDAYHLMPIKVLKVSSQVVAGMKYKMEIQVARSDCKKSSNEKI 108
154 CPDCPSPIDLSNPSALEAATESLAKFNSKSPSKKY-ELVKVTKAMNQWVSGPAYYVBYLI 212
 MEDLINE=22388257; PubMed=12477932; MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausher R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 25 ELEETLIHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESNEEL
 72 RETICSK-----ESNEELIESCEIKKLGQSLDCNAEVYVVPWEKKIYPIVNCQ 119
 13 KEAPCTKSQASCSLQHSDSEPVGICQGSTVQSSL--RHVPLIQPVEKSV--TVTCE 264
 Litomosoides sigmodontis.

Bukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea, Onchocercidae, Litomosoides.

NCBI_TaxID=42156;
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 N Fill

A PEAFE A.W., Hoffmann W.H., Taylor D.W., Schulz-Key H.;

A Pfaff A.W., Hoffmann W.H., Taylor D.W., Schulz-Key H.;

T Characterization and immunological properties of a cystein prot inhibitor of the filarial parasite Litomosoides sigmodontis.";

E Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

B RBL, ARZ29173, AAZ5896.1;

C GO; GO:0004889; F:systeine protease inhibitor activity; IEA.

DR FROW FFOOWER: cystein.

DR FROM FOOWER: cystein; 1.

DR SYMART; SW00043; Cy; 1.

DR PROSITE; PS00287; CYSTATIN; 1.

DR PROSITE; PS00287; CYSTATIN; 1.
 17.2%; Score 113.5; DB 5; Length 34.1%; Pred. No. 0.0011; ive 16; Mismatches 37; Indels
 01-00N-2003 (TrEMBLrel. 24, Created)
01-0UN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
 01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 109 DLKTC--KKLEGHPDQIITLEVWEKAWE 134
 85 -TESCETKKLGQSLD--CNAEVYVVPWE 109
 PRT;
 PRT;
 SEQUENCE 148 AA; 16686 MW;
 Best Local Similarity 34.1.8
Matches 30; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Cystatin-like 1
 Ls-cystatin.
 Q9NH95
Q9NH95;
 Q80Y72
 RESULT 13
Q9NH95
 RESULT 14
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 202 IMETNCTNKEAPQNEESCKALCGEKARYGFCKSTKVGIEEPBVECEIYEAKNITHFWKHP 261
 142 CPDCPGLLPLHDPKGLESVKTALQKFNKESDHKSYFKLMEVGRISTQWMFSGQSFFSQFA 201
 71 ARETICSKE---SNEELIES-----CETKKLG-OSLDCNAEVYVV----PWEKK 111
 12 CVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVA 71
 SEQUENCE FROM N.A.

CRAINE-225464; TISSUE-Vagina;

MEDLINE-22554683; PubMed=1246685;

The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

Thanlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.;

IL Malysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.;

IL MAILLE 420:563-573 (2002).

R MGD, MG:1800221; Fetub.

R MGD, MG:1800221; Fetub.

R MGD, MG:1800221; Fetub.

R InterPro; IPR00010; Cystatin.

R InterPro; IPR000116; Cystatin.

R Pfam; Pr00031; Cystatin; 2.
 οĘ
 CVGCPRDIPINSPELEETLIHTITKLNAENNATFYPKIDNVKKARVQ-VVAGKKYFIDFV
 Gaps
 20; Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 13;
 DB 11; Length 388;
 Teal P.-L., Chang G.-D., Huang C.-J.;
"Purification and cloning of carp fetuin.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY225965; AAD4662.1;
-GO; GO:0005874; C:microtubule; IEA.
GO; GO:0002199; F:cysteine protease inhibitor activity; IEA.
GO; GO:0007198; P:microtubule-based movement; IEA.
InterPro; IPR002453; Beta_tubulin.
InterPro; IPR00010; Cystatin.
 / Match 17.9%; Score 118; DB 13; Length 464; Local Similarity 24.2%; Pred. No. 0.0015; ses 31; Conservative 27; Mismatches 50; Indels 20
 48; Indels
 PROSITE; PS01254; PETUIN 1; 1.
PROSITE; PS01255; PETUIN 2; 1.
SPROSITE; PS A4; 42742 MW; 78CFAD73A8D8DC22 CRC64;
 PROSITE; PS00228; TUBULIN B AUTOREG; 1.
SEQUENCE 464 AA; 51698 MW; 7A54F71E44050895 CRC64;
 Last sequence update)
Last annotation update)
 17.5%; Score 115.5; DB 1
26.7%; Pred. No. 0.0022;
cive 24; Mismatches 46
 388 AA
 Created)
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
 Pfam; PF00031; cystatin; 1. SMART; SM00043; CY; 1.
 Query Match
Best Local Similarity 26.7%
Matches 31; Conservative
 PRELIMINARY;
 112 IYPTVNCQ 119
 262 AQSRRDČK 269
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 NCBI_TaxID=7962;
 Fetuin beta.
 12
 Query Match
 Q8CB17
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5; Gaps

DB 5; Length 148;

protease .";

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+4 INSTLHFFIRSYNNASNDTYLYQVQKLIQGQMQLTTGVEYLVTVKIGRTKCKK--NETKK 101
 26 LEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETTCSKESNEELT 85
 20 PINSPELEETLIHTIIKLMAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETICSKE 79
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
 Gaps
 Gaps
 Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
 4
 9;
 EMBL, BC048646, AA448646.1; -.
GO, GO:0004869; F:cysteine protease inhibitor activity, IEA.
InterPro, IPR00010; Cystatin.
InterPro, IPR003243; Cystatin_C/M.
 Length 140;
 16.8%; Score 111; DB 11; Length 146; 30.5%; Pred. No. 0.002; Live 18; Mismatches 42; Indels
 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027680; AAH27680.1; -.
InterPro; IDR00010; Cystatin.
Pfam; PF00031; cystatin; 1.
SMART; SM00043; CY; 1.
 Query Match 17.1%; Score 113; DB 11; Length 1 Best Local Similarity 29.4%; Pred. No. 0.0012; Matches 25; Conservative 18; Mismatches 38; Indels
 Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE 146 AA; 16380 MW; 9D77BB9A6063A5C4 CRC64;
 08K397;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
RIKEN CDNA 1110017E11 gene (Fragment).
 102 ASCPLOSSKLKKSLICKSLIYSVPW 126
 ESC--ETKKLGOSLDCNAEVYVVPW 108
 PRT;
 Query Match
Best Local Similarity 30.5%
Matches 29; Conservative
 PRELIMINARY;
 TISSUE=Mammary gland;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 rissum=Testicle;
 Pfam; PF0003
 Q8K397
 RESULT 15
Q8K397
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40 PTD-PRVQKAAQAAVASYNMGSDSLYYFRDTKVIDAKYQLVAGIKYYLTLDIESTECRKT 98

--SNEEL-TESCETKKLGQ--SLDCNAEVYVVPWE 109

80

g

```
99 RVSGEHMDLTTCPLAAGGQQEKLRCNFELLEVPWK 133
음
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Search completed: September 24, 2004, 14:10:17 Job time : 38.424 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
```

sw model - protein search, using OM protein September 24, 2004, 14:06:08; Search time 13.284 Seconds (without alignments) 890.662 Million cell updates/sec Run on:

Title: Perfect score:

US-10-661-784-1 660 1 GKDFVQPPTKICVGCPRDIP.......YVVFWEKKIYPTVNCQPLGM 123 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | ,          |        |    | SUMMARIES |                    |
|---------------|-------|------------|--------|----|-----------|--------------------|
| Result<br>No. | Score |            | Length | DB | ΙD        | Description        |
| :             | 999   | 100.0      | 427    |    | KGHUL1    | kininogen, LMW pre |
| 7             | 660   | 100.0      | 644    | Н  | KGHUH1    | kininogen, HMW pre |
| ų             | 477   | 72.3       |        | Н  | KGBOL1    | I.MW               |
| 4             | 477   | 72.3       | 62     | Н  | KGBOH1    | HMM                |
| ഗ             | 450   | 68.2       | 43     | Н  | KGBOL2    | LMW                |
| 9             | 450   | 68.2       |        | Н  | KGBOH2    | kininogen, HMW II  |
| . 7           | 426   | 64.5       | 43     | 7  | A28055    | K-kininogen, LMW I |
| œ             | 426   | 4          | 63     | N  | A25486    | kininogen, HMW I p |
| σ             | 409   | 62.0       | 43     | N  | A23897    | major acute phase  |
| 10            | 409   | $^{\circ}$ | 43     | N  | B28055    | T-kininogen, LMW I |
| 11            | 402   | 0          | 42     | Н  | KGRIM     | major acute phase  |
| 12            | 401   | 60.8       | 43     | ~  | KGRTT1    | T-kininogen I prec |
| 13            | 136   | 20.6       |        | Н  | UDBO      | cystatin - bovine  |
| 14            | 133   | 20.2       | σ      | N  | S68034    | T-kininogen (clone |
| 15            | 133   | 0          | 6      | N  | S68035    | T-kininogen (clone |
| 16            | 130   | σ          | 12     | ~  | S07085    | cystatin C precurs |
| 17            | 129   | σ          | 12     | N  | S10587    | U                  |
| 18            | 128   | 19.4       | 11     | N  | A28793    | cystatin - puff ad |
| 13            | 127.5 | 19.3       | 14     | N  | A36163    | υ                  |
| 20            | 127.5 | •          | 14     | Н  | חאמח      | υ                  |
| 21            | 125   | •          | 14     | ~  | B29632    | ω̈                 |
| 22            | 118.5 | •          | 13     | Н  | дрсн      |                    |
| 23            | 113.5 | •          | 12     | 7  | A43644    | u                  |
| 24            | 113   | ٠          | 14     | ~  | JQ1470    | CΩ                 |
| 25            | 111.5 | •          | 11     | Н  | JC2040    | ı                  |
| 56            | 109.5 | •          | 14     | Н  | UDHUP2    |                    |
| 27            | 109   | •          | 14     | Н  | UDHUP1    | cystatin S precurs |
| 78            | 107.5 | •          | 13     | ~  | JC4918    | cystatin precursor |
| 53            | 107   | ٠          | 13     | N  | T33740    | hypothetical prote |
|               |       |            |        |    |           |                    |

| onchocystatin - ne | cystatin II - maiz | cystatin precursor | hypothetical prote | cystatin D precurs | cystatin-related e | alpha-2-HS-glycopr | cystatin - avocado | . cysteine proteinas | fetuin precursor - | cysteine proteinas | cysteine proteinas | cystatin - maize | alpha-2-HS-glycopr | cystatin - field m | Ca2+ dependent lip |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|
| A43428             | JC4007             | JC4536             | T33301 ·           | A47142             | A45361             | S21094             | JH0269             | S27239               | A32827             | T00752             | S54828             | JC4882           | WOHU               | S65071             | T50516             |
| C)                 | (1                 | ~                  | 0                  | (7)                | N                  | N                  | 7                  | 7                    | N                  | N                  | 7                  | N                | Н                  | ~                  | 7                  |
| 162                | 135                | 133                | 143                | 142                | 139                | 345                | 100                | 135                  | 375                | 125                | 134                | 134              | 367                | 199                | 592                |
| 16.0               | 14.8               | 14.7               | 14.5               | 14.4               | 14.2               | 14.2               | 13.9               | 13.9                 | 13.7               | 13.4               | 13.4               | 13.4             | 13.0               | 12.9               | 12.8               |
|                    |                    | 97                 | 'n                 | 95                 | ď.                 | .5                 | 92                 | 1.5                  | 0.5                | 88.5               | 8.5                | ю<br>го          | 5.5                | 85                 | 84.5               |
| 105.5              | 97.5               | Ο,                 | 95                 |                    | 93                 | 9                  |                    | g                    | ō                  | ω                  | ω                  | æσ               | æ                  |                    | à                  |

# ALIGNMENTS

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|----|---|
| H  | - |
| 뎚  | E |

Kininogen, LMW precursor [validated] - human

Kininogen, LMW precursor [validated] - human

NyAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen

NyAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen

Cybaceiss: Homo sapiens (man)

Cybaceission: All 1982 #sequence revision 27-Nov-1985 #text change 08-Dec-2000

Cybaceission: All 280

AyTitle: Esolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identi

AyReference number: A90490; MUD:88122621; PMD:6441591

AyAccession: All 280

AyAccession: All 280

AyAccession: All 280

AyAccession: All 280

AyAccession: Bacarence analysis of cDNAs for human high molecular weight and low

AyEference number: A92544; MUD:85234582; PMD:2989293

AyAccession: B25276

AyAccess

A; Accession: A27900 A; Molecule type: protein A; Residues: 390-427 < LOT-> R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scioli, A.G. Biochem. Blophys. Res. Commun. 152, 519-526, 1998 A; Title: A new Kinin moiety in human plasma kininogens. A; Reference number: A27699; MUID:88209021; PMID:3365237

A;Molecule type: protein
A;Molecule type: protein
A;Meadduce: 180-1399 <MIN.
A;Residuce: 180-1399 <MIN.
A;Residuce: 180-1399
J. Biol. Chem. 263, 16051-16054, 1998
J. Biol. Chem. 263, 16051-16054, 1998
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic flui A;Reference number: A31905; MUID:89034061; PMID:3182782
A;Accession: A31905

A;Molecule type: protein

A;Molecule type: protein

R;Residues: 38.1-389 eAM.;

R;Sasaguri, M.; Ideishi, M.; Arakawa, K.

Biochem. Biophys. Res. Commun. 150, 511-516, 1988

Biochem. Biophys. Res. Commun. 150, 511-516, 1988

A;Title: dentification of [hydroxyprolline(3)]-lysyl-bradykinin released from human plas:
A;Reference number: A34030, MUID:88106632; PMID:3337729

A;Molecule type: protein A;Residues: 380-389 <SAS>

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A; Experimental source: urine
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 ;Accession: A27699
 A;Accession: S02482
 A;Accession: A61495
 A; Accession: A24871
 Accession: A27899
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S. J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evoluti A;Reference number: A92545; MUID:852483; PMID:2989294
A;Contents: annotation; gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A9455; MUID:90255622; PMID:4952632
A;Contents: annotation; bradykinin
C;Comment: The Luw kininogen precursor is produced from the same gene as the HWW form (6 C;Comment: The Luw kininogen precursor is produced from the same gene as the HWW form (6 C;Comment: Endykinin, released from kininogen by kallikrein, is a potent vasodilator, ixporoline residue is present in the kininogen by kallikrein, is a potent vasodilator, ixporoline residue is present in the kininogen prior to the release of bradykinin.
C;Genetics:
A;Gene: GDB:KNG
A;Cross-references: GDB:125256; OMIM:228960
A;Map position: 3427-3427
A;Introns: 5679; 102/3; 131/1; 18873; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
C;Superfamily: kininogen; cystetin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc;Fil-18/Domain: signal sequence #steuus predicted <AMT>
F;19-389, 390-427/Product: LWW kininogen II #status predicted <AMT>
F;19-31/Domain: cystatin homology <CV2>
F;19-13/Domain: cystatin homology <CV2>
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Kininogen, HMW precursor [validated] - human
Kininogen, HMM kininogen; prokininogen
Kininogen II; low molecular we
Cipsecies: Homo sapiens (man)
Cipsecies: Homo sapiens
Kiokubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identianane number: A90490; MUD:85122621; PMID:6441591
A; Residues: Lype: mRNA
A; Molecule type: MRNA
A; MRNA
A; Molecule type: MRNA
A; Molecule t
 F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
F;264-375/Domain: cystatin homology <CY3>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
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F;390-427/Product: Lyw kininogen light chain #status experimental <LCHP
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F;380-437/Product: Lyw kininogen light chain #status predicted
F;28-407,83-94,107-126,142-145,206-218,289-48,264-267,328-340,351-370/Disulfide bonds:
F;89,169,205,294/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;393-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 ö
 253 GKDFVQPPTKICVGCPRDIPTNSPELETLIHTITKLNAENNATFYPKIDNVKKARVQVV 312
 61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 9
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
 Gaps
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 Length 427;
 F;389-390/Cleavage site: Arg-ver (Ahr) (covalent) #status absent
 Indels
 100.0%; Score 660; DB 1;
100.0%; Pred. No. 3.3e-55;
ive 0; Mismatches 0;
 Query Match 100.
Best Local Similarity 100.
Matches 123; Conservative
 121 LGM 123
 LGM 375
 373
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A;Molecule type: protein
A;Residues: 380-389 cMIN>
R;Maeda, H.; Matsumura, Y.; Kato, H.
B;Datl. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic fluich;A;Reference number: A31905; MUID:89034061; PMID:3182782
A;Accession: A31905
 A,Molecule type: protein
A,Molecule type: protein
A,Residues: 381-389 cMB.
R,Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
R,Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
Biochem. Gonthication of [hydroxyprolline(3)]-1ysyl-bradykinin released from human plasm
A,Reference number: A34030; MUID:88106632; PMID:3337729
A,Accession: A34030
 A;Molecule type: protein
A;Residues: 'Z',20-380 «KEL1>
R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
In Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New Yorl
A;Title: Amino acid sequence of the light chain of human high molecular mass kininogen.
A;Reference number: A27899
 A; Molecule type: mRNA
A; Residues: Angry, 253-377 < AUE>
A; Residues: AIRM, 253-377 < AUE>
A; Note: differences are due to known cloning artifacts
R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
R; Lottspeich, F.; Kellermann, J.; 1985
A; Title: The amino acid sequence of the light chain of human high-molecular-mass kininoge
A; Reference number: A91153; MUID: 86030270; PMID: 4054110
 (CPIs) in inflammatory and
 Jitle: Isolation and identification of hydroxyproline analogues of bradykinin in human, Reference number: A61495; MUD:88211869; PMID:3366244
 The
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
A;Reference number: A92544; MUID:85234582; PMID:2989293
A;Accession: A25276
 A,Molecule type: protein
A,Residues: 379-644 (LOID)
A,Residues: 379-644 (LOID)
A,Note: the bradykinin sequence preceding the light chain sequence was not determined
R,Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
Eur. J. Blachem. 154, 471-478, 1196
Eur. J. Blachem. 154, 471-478, 1196
A,Title: Completion of the primary structure of human high-molecular-mass kininogen. T
A,Reference number: A24871; MUID:86108361; PMID:3484703
 A; Molecule type: mRNA
A; Residues: 1-592, 1', 594-644 < TAK>
A; Cross-references: GB:M11437; NID:G186751; PIDN:AAB59550.1; PID:G386852
A; Cross-references: GB:M11437; NID:G186751; PIDN:AAB59550.1; PID:G386852
R; Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.
FEBS Lett. 321, 93-97, 1993
A; Title: CLOning, expression and characterization of human kininogen domain 3.
A; Reference number: $32422; MUID:93223854; PMID:8467916
 Š
 M.; Turk,
 A;Molecule type: protein
A;Residues: 379-389, 'K',390-407,'O',409-644 <KEL2>
A;Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988.
A;Tille: A new kinin moiery in human plasma kininogens.
A;Reference number: A27699; MUID:88209021; PMID:3365237
 A;Molecule type: protein
A;Residues: 380-389 <SAS>
R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, I
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
Biol. Human cathepsin B and cysteine proteinase inhibitors
A;Title: Human cathepsin B and cysteine proteinase inhibitors
A;Reference number: S02482; MUID:89076517; PMID:3264507
 A;Molecule type: protein
A;Residues: 1-19;189-192;310-314;381-389 <LENI>
 A;Residues: 1-19;189-192;310-314;381
R;Karo, H.; Mataumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A;Title: Isolation and identificatio
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Gaps

Mon

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A; Krestauces: 1435 CAMA,
A; Cross-references: GB:J00010; GB:V00426; NID:g163256; PIDN:AAA30604.1; PID:g163257
C; Comment: The LMW kininogen precursor is produced from the same gene as the HWW form as C; Comment: Kininogen is a cysteine proteinase inhibitor; takes part in initiation of the C; Comment: Kininogen; as a cysteine protein by kallikrein, is a potent vasodilator, i xyproline residue is present in the kininogen by kallikrein, is a potent vasodilator, i xyproline residue is present in the kininogen prior to the release of bradykinin.
C; Superfamily: Kininogen; cystatin homology
C; Superfamily: Kininogen i #status predicted «KMT»
F; 19-436/Product: LMW kininogen I #status predicted «KMT»
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F; 389-346/Product: LMW kininogen I heavy chain #status predicted companien: cystatin homology «CYI»
F; 389-386/Product: LMW kininogen I light chain #status predicted companien: cystatin homology companien: cystatin cy
 C;Accession: A01283
R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors
A;Reference number: A93984; MUID:83117859; PMID:6572010
 253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312
 61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); Kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle) (C;Species: Bos primigenius taurus (cattle) (C;Species: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
 62 GKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPL
 313 AGKKYPIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVVVPWEKKIYPTVNCQP
 KDFVQPPTKI CVGCPRDI PTNSPELEETLTHTITKLNAENNATFYFKI DNVKKARVQVVA
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 Length 644;
 Length 436;
 Indels
 20;
 Score 660; DB 1;
Pred. No. 5.1e-55;
Mismatches 0;
 Query Match 72.3%; Score 477; DB 1; Best Local Similarity 71.9%; Pred. No. 9.2e-38; Matches 87; Conservative 14; Mismatches 20
 ;
0
 100.0%;
 Conservative
 A, Accession: A01283
A, Molecule type: mRNA
A, Residues: 1-436 < NAW>
 Similarity
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 121 LGM 123
 122 G 122
 373
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A. Note: the petide had Pro-181 modified to 4-hydroxyproline
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Gaps

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72.3%;
 87; Conservative
 84; Conservative
 LMW II precursor -
 Query Match
Best Local Similarity
 A; Molecule type: mRNA
A; Residues: 1-434 <NAW>
 Local Similarity
 LG 122
 122 G 122
 373 G 373
 121
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 A,Title: A single gene for bovine high molecular weight and low molecular weight kininog
A,Reference number: A93317; MUID:84014106; PMID:6571699
 A,Accession: A91923
A,Molecule type: protein
A,Residues: 378-393 «KAT»
R;Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.
B,Blochem. 77, S5-68, 1975
A,Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami
A,Reference number: A91938; MUID:75170265; PMID:1169237
 cleavages of disulfide bonds and
 A; Molecule type: mRNA
A; Residues: 1-621 «KIT>
A; Cross-references: GB: V01491; GB: K01757; NID: g491; PIDN: CAA24735.1; PID: g492
R; Kato, H.; Nagasawa, S.; Suzuki, T.
J. Blochem. 67, 313-232, 1970
A; Fitle: Studies on the structure of bovine kininogen: cleavages of disulfide
A; Reference number: A91923; MUID: 70180420; PMID: 4986212
N'Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N'Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01281, A31923; A31938; A29559
R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S Nature 305, 545-549, 1983
 A;Accession: A01281
```

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A,rcross-references: GB:V00427, GB:J00011; NID:g489; PIDN:CAA23710.1; PID:g490
A,rcross-references: GB:V00427, GB:J00011; NID:g489; PIDN:CAA23710.1; PID:g490
C,Comment: The LWW kininogen precursor is produced from the same gene as the HWW form as C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, in xyproline residue is present in the kininogen by kallikrein, is a potent vasodilator, in xyproline residue is present in the kininogen prior to the release of bradykinin. C;Superfamlly: kininogen: cystatin homology
C;Superfamlly: kininogen: cystatin homology
C;Kyproduct: LWM kininogen II #status predicted <AGA>
F;19-434/Product: LWM kininogen II #status predicted <AGA>
F;19-130/Domain: cystatin homology <CY2>
F;10-130/Domain: c
 (covalent) #status exp
 Rinawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A;Title: Primary structures of bovine liver low molecular weight kininogen precursors and A;Reference number: A93984; MUID:83117859; PMID:6572010
A;Accession: A01284
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 309
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 369
 312
 62 GKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQPL 121
 372
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 N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle) C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999 C;Accession: A01284
 KDFVQPPTKI CVGCPRDI PTNSPELEETLTHTITKLNAENNATFYFKI DNVKKARVQVVA
 313 GLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVVVVWHEEKVYPTVNCQPL
 252 GEDFL--PPMVCVGCPKPIPVDSPDLEEALNHSIAKLNAEHDGTFYFKIDTVKKATVQVV
 61 AGXKYPIDFVARETICSKESNEELIESCETKGLGQSLDCNAEVYVVPWEKKIYPTVNCQP
 310 GGLKYSIVFIARETTCSKGSNEELTKSCEINIHGQILHCDANVYVVFWEEKVYPTVNCQP
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
 Gaps
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 ;
F;398,406,512/Binding site: carbohydrate (Ser) (covalent) #status (
F;399,400,520,524,536,548,553,570/Binding site: carbohydrate (Thr)
F;498-499/Cleavage site: Arg-Thr (kallikrein) #status experimental
 68.2%; Score 450; DB 1; Length 434; 68.9%; Pred. No. 3.4e-35; ive 14; Mismatches 22; Indels
 Length 621;
 Indels
 20;
 Score 477; DB 1;
Pred. No. 1.4e-37;
 14; Mismatches
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Gaps

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F/387-619/Product: HTM kininogen II light chain #status experimental <LCH>
F/18-48/Region: glycine/histidine/lysine-rich
F/18-48/Region: glycine/histidine/lysine-rich
F/19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F/27-89, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:
F/27/Rinding site: carbohydrate (Asn) (covalent) #status absent
F/18/Rinding site: carbohydrate (Asn) (covalent) #status experimental
F/19/Rinding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F/19/Rinding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F/19/Rinding site: carbohydrate (Asn) (covalent) #status experimental
F/19/Rinding site: carbohydrate (Asn) (covalent) #status experimental
F/19/Rinding site: carbohydrate (Asn) (covalent) #status experimental
F/19/Rinding site: Arg-Ser (kallikrein) #status predicted
F/19/F/10-84996 site: Arg-Ser (kallikrein) #status experimental
F/19/F/10-84996 site: Arg-Thr (kallikrein) #status experimental
F/19/F/10-84996 site: Arg-Thr (kallikrein) #status experimental
 R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
 61 AGKKYFIDFVARETICSKESNEBLIESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 310 GGLKYSIVFIARETTCSKGSNBELIKSCEINIHGQILHCDANVZVVPWEEKVYPTVNCQP 369
 61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
 GKDFVQPPTKICVGCPRDIPTNSPBLEBTLTHTITKLNABNNATFYFKIDNVKKARVQVV
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
 0; Gaps
;378-386/Product: bradykinin (kallidin I) #status experimental <BDY>
 2
 Length 433;
 Length 619;
 Query Match 68.2%; Score 450; DB 1; Length 61
Best Local Similarity 68.9%; Pred. No. 5.1e-35;
Matches 84; Conservative 14; Mismatches 22; Indels
 29; Indels
 <MAT>
 A; Reference number: A92496; MUID:86008264; PMID:2413018
 A, Molecule type: mRNA
A, Residues: 1-433 < FUR>
C, Superfamily: kininogen; cystatin homology
C, Superfamily: kininogen; cystatin homology
C, Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-433/Product: K-kininogen, LMW I #status predicted
F;19-131/Domain: cystatin homology <CX2>
F;264-253/Domain: cystatin homology <CX2>
F;264-375/Domain: cystatin homology <CX3>
 64.5%; Score 426; DB 2;
65.0%; Pred. No. 6.6e-33;
 14; Mismatches
 K-kininogen, LMW I precursor - rat
 Conservative
 Query Match
Best Local Similarity
Matches 80; Conserv
 LDM 375
 121 LGM 123
 121 LG 122
 LG 371
 C; Accession: A28055
 A; Accession: A28055
 373
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 LG 371
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15; Mismatches
 A;Wolecule type: protein
A;Residues: 'E',20-25,'MD',28-48,376-430 <ENJ>
A;Accession: C28526
 62.0%;
 Query Match
Best Local Similarity 61.8*
Matches 76; Conservative
 LGM 123
 372 LDM 374
 121 LGM 123
 372 LDM 374
 A; Accession: B28526
 121
 nhibitor.
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 A;Molecule type: mRNA
A;Residues: 5-430 cAND2>
A;Residues: 5-430 cAND2>
A;Cross-references: GB:M11661; NID:g205307; PIDN:AAA41570.1; PID:g205308
A;Cross-references: GB:M11661; NID:g205307; FIDN:AAA41570.1; PID:g205308
C;Superfamily: kininogen; cystatin homology
F;19-130/Domain: cystatin homology cY12>
F;14-125/Domain: cystatin homology cY15
F;263-374/homain: cystatin homology
 gene family.
 A23897

major acute phase alpha-1 protein (version 2) - rat

C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C;Accession, A23897, B23897
J; Heath, B.C.
J; Biol. Chem. 260, 12065-12071, 1985
A;Tille: The relationship between rat major acute phase protein and the kininogens.
A;Reference number: A23897; MUID:86008266; PMID:2413019
A25486
Kininogen, HWW I precursor - rat
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A25486
C;Accession: A25486
R;Kitaqawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
J;Fitle Differing expression patterns and evolution of the rat kininogen gene f
A;Reference number: A92625; MUID:87137443; PMID:3029068
A;Accession: A25486
A;Reference number: A52625; MUID:87137443; PMID:3029068
A;Reference number: A52625;
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 253 GDDLFELLPEDCPGCPRNIPVDSPELKEALGHSIAQLNAENNHTFYFKIDTVKKATSQVV 312
 61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 313 AGTKYVIEFIARETKCSKESNAELTADCETKRLGQSLNCNANVYMRPWENKVVPTVKCKV 372
 252 GDDLFSLLPKKCPGCPKNIPVDSPELKEALGHSIAQLNAQHNHLFYPKIDTVKKATSQVV 311
 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 312 AGTKYVIEFIARETNCSKQTNTBLTADCETKHLGGSLNCNANVYMRPWENKVVPTVRCQA 371
 9
 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTTTKLNAENNATFYFKIDNVKKARVQVV
 0; Gaps
 ö
 Query Match 64.5%; Score 426; DB.2; Length 639; Best Local Similarity 65.0%; Pred. No. 1e-32; Matches 80; Conservative 14; Mismatches 29; Indels
 62.0%; Score 409; DB 2; Length 430; 61.8%; Pred. No. 2.7e-31; Live 15; Mismatches 32; Indels
 Superfamily: kininogen; cystatin homology Jb-130/Domain: cystatin homology <CY1>141-252/Domain: cystatin homology <CY2>;263-374/Domain: cystatin homology <CY3>
 F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
 Query Match
Best Local Similarity 61.8%
Matches 76; Conservative
 121 LGM 123
 LDM 375
 373
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A; Molecule type: protein
A; Molecule type: protein
A; Residues; 'E'. 20-48;376-388, 'R', 390-419, 'ER', 422-430 <EN2>
C; Superfamily: kininogen; cystatin homology
C; Reywords: glycoprotein; pyroglutamic acid
F;19-430, Product: T-kininogen, LMM II #status experimental <MAT>
F;19-430, Product: T-kininogen, LMM II #status experimental <MAT>
F;19-430, Product: T-kininogen, CY12>
F;19-130, Promain: cystatin homology <CY2>
F;19-100main: cystatin homology <CY2>
F;19-100main: cystatin homology <CY3>
F;19-100main: cystatin homology <CY3>
F;19-100main: cystatin homology <CY3>
F;10-100main: cystatin homology <CY3-
F;10-100main: cystatin homol
T-kininogen, LMW II precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: 20-Jun-1989 #sequence revision 20-Jun-1989 #text_change 12-Dec-1997
C.Accession: B28055; E25486; B28526; C28526
C.Accession: A28055; E25486; B28526; C28526
C.Accession: J228055; A38040000, A.; Kitemura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A; Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
 A;Molecule type: DNA
A;Residues: 375-430 «KIT»
A;Residues: 375-430 «KIT»
A;Riyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
Biol. Chem. 263, 973-979, 1988
A;Title: Purification and characterization of rat T-kininogens isolated from plasma of A;Reference number: A92729; MUID:88087226; PMID:3121623
 A; Accession: B28055.
A; Molecule type: mRNA
A; Residues: 1-430 <FUR>
B; Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 1390-2198, 1387
A; Tille: Differing expression patterns and evolution of the rat kininogen gene family. A; Reference number: A$2625; MUD:87137443; PMID:3029068
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 311
 61 AGKKYFIDFVARETTCSKESNEBLTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 312 AGTKYVIEFIARETNCSKQTNTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA 371
 9
 major acute phase alpha-1 protein precursor - rat (fragment)
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
C;Accession: A01285
R;Cole, T; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
 252 GDDLFSLLPKKCFGCPKNIPVDSPELKEALGHSIAQLNAQHNHLFYFKIDTVKKATSQVV
 Gaps
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 Length 430;
 32; Indels
 A; Reference number: A92496; MUID: 86008264; PMID: 2413018
 Score 409; DB 2;
Pred. No. 2.7e-31;
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N'Alternate names: 73K procein; LWW kininogen T-I
N'Alternate names: 73K procein; LWW kininogen T-I
N'Alternate names: 73K procein; LWW kininogen T-I
N'Alternate names: 73K procein; LWM Contains bradykinin; T-Xinin
C'Species: Rattus norvegicus (Norvay rat)
C'Date: 17-Mar-1997 #sequence_revision 17-Mar-1997 #REX. Change 22-Uun-1999
C'Accession: Alloso; D2486; A2826; PL0193; aC0027; D25488; A2825; S68036
N'ALTICLE: Primary structures of the mRNAs encoding the rat precursors for bradykinin and nhibitor.
A'RELE: Primary structures of the mRNAs encoding the rat precursors for bradykinin and nhibitor.
A'RECTOR: 260, 12084-12085.
A'RICLE: Primary structures of the mRNAs encoding the rat precursors for bradykinin and hibitor.
A'RECTOR: 262, 1209-1208.
A'RICLE: D16FE-1076 *REX.
A'RECTOR: 262, 1209-1208, 1304
A'RECTOR: 262, 1209-1208
A'RECTOR: 262, 1209-1209
A'RECTOR: 262, 1200-1209
A'RECTOR: 262, 1200-1200
A'RECTOR: 262, 1200-1200
A'RECTOR: 262, 1200
A'RECTOR: 262, 1
A.Title: Major acute phase alphal-protein of the rat is homologous to bovine kininogen a A.Reference number: A01285, MUD:85127561; PMID:2578992
A.Rocessabon: A01285
A.Rocessabon
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 61 AGKKYFIDFVARETICSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCQP 120
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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 Query Match 60.9%; Score 402; DB 1; Length 423; Best Local Similarity 61.8%; Pred. No. 1.2e-30; Matches 76; Conservative 14; Mismatches 33; Indels
 121 LGM 123
 LDM 367
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A; Intrones: 65/3; 102/3; 130/1; 187/3; 223/2; 255/1; 309/3; 345/3; 374/3; 398/3
C; Superfamily: kininogen; cystatin homology
C; Seywords: acute phase; bradykinin; cysteline proteinase inhibitor; duplication; glycopr E; 1-18/Domain: signal sequence #status predicted <SIG>P; 19-130/Domain: signal sequence #status predicted <SIG>P; 19-130/Domain: cystatin homology <CYI>P; 19-130/Domain: cystatin homology <CYI
P; 19-130/Domain: cystatin homology
 A;Accession: 000027

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-60, K', 62-113, K',115-165, F',167-178, TKI',182-211, F',213-256, S',258-386

A;Experimental source: strain Sprague-Dawley

R;Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.

B;Ol. Chem. 252, 2345-2351, 1987

A;Title: Differing utilization of homologous transcription initiation sites of rat K and

A;Reference number: A25488; MUID:87137465; PMID:3818598
 'Status: preliminary
'Molecule type: DNA
'Rolecule type: DNA
'Rolecule type: DNA
'Cross-references: 1.48 «KAG>
'Cross-references: GB:M14356; NID:g205090; PIDN:AAA41492.1; PID:g205091
'Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
Biol. Chem. 263, 965-972, 1988
'Title: Purification and characterization of two kinds of low molecular weight kininoge: 'Reference number: A28525; MUID:88087225; PMID:333530
 C;Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after d of an Arg or Lys, it is probably not released from its precursor by either tissue or C;Comment: The T-kininogens are produced in response to an inflammatory stimulant. C;Genetics:
 A;Molecule type: mRNA
A;Residues: 340-430 <SIE>
A;Experimental source: clone pSG17
C;Comment: At least three types of LMW kininogen precursors are present in rat plasma,
ceding bradykinin.
 i,Molecule type: protein
ty,Residues: 376-430 <EN2>
ty,Residues: 376-430 <EN2>
ty,Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
trch. Biochem. Biophys. 322, 333-338, 1995
ty,Title: Identification of several isoforms of T-kininogen expressed in the liver of ty,Reference number: S68034; MUID:96032652; PMID:7574705
 61 AGKKYFIDFVARETICSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 9
 1 GKDFVQPPTKICVGCPRDIPTNSPBLBETLTHTITKLNAENNATFYFKIDNVKKARVQVV
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0
 Length 430;
R;Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A;Title: Primary structure of a gene encoding rat T-kininogen.
A;Reference number: JQ0027; MUID:90034172; PMID:2806908
 33; Indels
 60.8%; Score 401; DB 1;
llarity 61.8%; Pred. No. 1.6e-30;
Conservative 14; Mismatches 33.
 proteinase inhibitor
 cystatin - bovine
N;Alternate names: thiol
 Local Similarity
ses 76; Conserv
 121 LGM 123
 LDM 374
 Accession: B25488
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Indels

Pred. No. 9.8e-06; 3; Mismatches 8;

68.6%;

Best Local Similarity 68.6 Matches 24; Conservative

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89 ETKKLGÓSLDCNAEVYVVPWEKKIYPTVNCQPLGM 123
 1 ETKHLGGSLNCNANVYMRPWENKVVPTVRCQALDM 35
 Search completed: September 24, 2004, 14:10:48 Job time : 14.284 secs
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 a
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 06-Dec-1996
C;Accession: A01271
R;Hirado, M.; Tsunasawa, S.; Sakiyama, F.; Niinobe, M.; Fujii, S.
FEBS Lett. 186, 41-45, 1985
A;Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase in A;Reference number: A01271; MUID:85231205; PMID:3891407
 T-kininogen (clone pSG17) - rat (fragment)
C.Species: Rattus norvegicus (Norway rat)
C.Joace: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
C.Accession: S68035
R.Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Blochem. Blophys. 322, 333-338, 1995
A.Jitle: Identification of several isoforms of T-kininogen expressed in the liver of agi
 Risierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A; Title: Identification of several isoforms of T-kininogen expressed in the liver of agi
A; Reference number: $68034; MUID:96032652; PMID:7574705
A; Accession: $68034
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 22 NSPELEETLTHTITKLNAENNATFYPKIDNVKKARVQVVAGKKYFIDFVARETTCSKESN 81
 T-kininogen (clone pSG22) - rat (fragment)
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C;Date: 12-Feb_1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
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A;Residues: 1-91 <SIE>
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C;Keywords: alternative splicing; cysteine proteinase inhibitor; plasma
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A; Experimental source: liver
C; Superfamily: kininogen; cystatin homology
C; Keywords: alternative splicing; cysteine proteinase inhibitor; plasma
 82 BELTESC-----ETKKLGQSLDCNAEVYVVPWEKKIYPTVN-----CQ 119
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 Length 112;
 Length 91;
 Score, 133; DB 2; Length 91;
 31; Indels
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68.6%; Pred. No. 9.8e-06;
tive 3; Mismatches 8;
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A; Molecule type: protein
A; Residues: 1-112 < 4112
C; Superfamily: cystatin; cystatin homology
C; Keywords: colostrum; cystaine proteinase inhibitor
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F; 48-82 / Residue: cystatin homology < cys.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SIMMARIES

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|------------|-------------------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|
|            | Description                   | Sequence 82, Appl | 70,              | Sequence 29, Appl | Sequence 72, Appl | Sequence 74, Appl | Sequence 84, Appl | Sequence 217, App | Sequence 215, App | Sequence 1, Appli | Sequence 2, Appli | Sequence 197, App | Sequence 14, Appl | Sequence 12, Appl |                 | Sequence 16, Appl |
| CONTRACTES |                               | US-10-162-335-82  | US-10-162-335-70 | US-09-919-039-29  | US-10-162-335-72  | US-10-162-335-74  | US-10-162-335-84  | US-10-316-253-217 | US-10-316-253-215 | US-09-969-834-1   | US-10-329-428-2   | US-09-746-783-197 | US-09-775-932-14  | US-09-775-932-12  | US-09-940-497-2 | US-08-849-303-16  |
|            | h DB                          | 0 15              | 8 15             | 2                 | 15                | 15                | 15                | 14                | 14                | σ                 | 14                | 2                 | σ                 | თ<br>თ            | о<br>О          | 2                 |
|            | o<br>Query<br>Match Length DB | 39                | 39               | 427               | 61                | 64                | 64                | 42                | 43                | 17                | 14                | 16                | 12                | 12                | 14              | 11                |
| d          | Query<br>Match                | 100.0             | 100.0            | 100.0             | 100.0             | 100.0             | 100.0             | 6.09              | 8.09              | 25.6              | 25.1              | 25.1              | 21.0              | 21.0              | 21.0            | 20.6              |
|            | Score                         | 660               | 099              | 099               | 099               | 660               | 099               | 402               | 401               | 169               | 165.5             | 165.5             | 138.5             | 138.5             | 138.5           | 136               |
|            | Result<br>No.                 |                   | 7                | m                 | 4                 | ហ                 | 9                 | 7                 | œ                 | თ                 | 10                | 11                | 12                | 13                | 14              | 15                |

| Sequence 16, Appl<br>Sequence 24, Appl<br>Sequence 19, Appl<br>Sequence 19, Appl<br>Sequence 48, Appl<br>Sequence 87, Appl<br>Sequence 80, Appl<br>Sequence 91, Appl<br>Sequence 78, Appl<br>Sequence 26, Appl<br>Sequence 26, Appl<br>Sequence 26, Appl<br>Sequence 26, Appl<br>Sequence 27, Appl<br>Sequence 18, Appl<br>Sequence 17, Appl<br>Sequence 18, Appl<br>Sequence 18, Appl<br>Sequence 17, Appl<br>Sequence 3, Appli<br>Sequence 17, Appli | - 4        |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|
| 0.05-03-03-03-03-03-03-03-03-03-03-03-03-03-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 141        |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |
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| 11111000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 4 4<br>4 C |

### ALIGNMENTS

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Sequence 82, Application US/10162335
Publication No. US20040009480A1
GENERAL INPORMATION:
APPLICANT: Anderson, David W.
APPLICANT: Balmgartner, Jason C.
APPLICANT: Balmgartner, Jason C.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gengolli, Esha A.
APPLICANT: Gengolli, Esha A.
APPLICANT: Gengolli, Esha A.
APPLICANT: Gengolli, Esha A.
APPLICANT: Gengolli, Tord
APPLICANT: MacDougall, John R.
APPLICANT: Hight, Tord
APPLICANT: Hight, Tord
APPLICANT: Hight, Tord
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: Sabelle
APPLICANT: Shimkets, Usidelle
APPLICANT: Shimkets, Rachard A.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B
CURRENT FILING DATE: 2001-06-04
FRIOR FILING DATE: 2001-06-04
FRIOR FILING DATE: 2001-06-04
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Sequence 29, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE PREFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
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PRIOR PILING DATE: 2000-07-28
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FEATURE:
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Best Local Similarity
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 344 LGM 346
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 US-09-919-039-29
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 APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Caryan D.
APPLICANT: Serbusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method FILE REFERENCE: 21402-377 B
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; Publication No. US20040009480A1
; GENERAL INFORMATION;
 Bungartner, Jason C.
Boldog, Ferenc L.
Casman, Stacte J.
Bdinger, Shlomit R.
Gangolli, Bsha A.
Gerlach, Valerie
Gorman, Linda
Guo, Xiaojia (Sasha)
Hjalt, Tord
 MacDougall, John R.
Malyankar, Uriel M.
Millet, Isabelle
Padigaru, Muralidhara
 Patturajan, Meera
Pena, Carol B. A.
Rastelli, Luca
Shimkets, Richard A.
 APPLICANT: Anderson, David W.
 TYPE: PRT
ORGANISM: Homo sapiens
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 JS-10-162-335-82
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LENGTH: 390
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 336
 APPLICANT
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APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, David Z.
APPLICANT: Vernet, 100 M. M.
APPLICANT: Vernet, 100 M. M.
IIILE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method FILE REPERENCE: 21402-37 B
CURRENT APPLICATION WUMBER: 60/295,607
PRIOR APPLICATION NUMBER: 60/295,61
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
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PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-12
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PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/290,949
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Matches 123; Conservative 0; Mismatches 0;
 Sequence 74, Application US/10162335
Publication No. US20040009480A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gangoll, Esha A.
APPLICANT: Gangoll, Esha A.
APPLICANT: Gorman, Linda
 Li, Li,
MacDougall, John R.
Malyankar, Uriel M.
Millet, Isabelle
Padigaru, Muralidhara
Patturajan, Meera
Pena, Carol E. A.
Rastelli, Luca
Shimkets, Richard A.
Stone, David J.
Spytek, Kimberly A.
Vernet, Corine A. M.
; ORGANISM: Homo sapiens
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 셤
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APPLICANTY MAJORAR, Unial M.
APPLICANTY MAJORAR, Unial M.
APPLICANTY MAJORAR, Unial M.
APPLICANTY MAJORAR, Unial M.
APPLICANTY Pand, Carol E. A.
APPLICANTY Pena, Carol E. A.
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APPLICANTY CAROL STRIPLY A.
APPLICANTY CAROL MAGNETIA M.
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 RESULT 4
US-10-162-335-72
Sequence 72, Application US/10162335
Publication No. US20040009480A1
SEGNERAL INFORMATION:
APPLICANT: Baungartner, Jason C.
APPLICANT: Boldog, Ferror L.
APPLICANT: Boldog, Ferror L.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gargolli, Esha A.
APPLICANT: Gargolli, Esha A.
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Groman, Linda
APPLICANT: Groman, Linda
APPLICANT: Growan, Linda
APPLICANT: Growan, Linda
APPLICANT: Growan, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
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 313 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372
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PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/298,556
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-26
REMAINING PRIOR FOR FACTOR NUMBER: 60/300,883
PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 84
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 Length 424;
 Query Match 60.9%; Score 402; DB 14; Length 4: Best Local Similarity 61.8%; Pred. No. 1.1e-35; Matches 76; Conservative 14; Mismatches 33; Indels
 JOHNSTON LINE PROCESS & Gamble Company
APPLICANT: The Process & Gamble Company
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
 Sequence 217, Application US/10316253
Publication No. US20030162706A1
GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
SEQ ID NO 217
) TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-217
 ; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-84
 121 LGM 123
 373 LGM 375
 121 LGM 123
 366 LDM 368
 US-10-316-253-217
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 APPLICANT: SUCHE, Kimberly A.
APPLICANT: SUCHE, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Voss, Edward Z.
APPLICANT: Lord State Corine A. M.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method FILE REFERENCE: 21402-377 B
CURRENT APPLICATION NUMBER: 60/295,607
PRIOR APPLICATION NUMBER: 60/295,601
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
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PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-01
PRIOR PELING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PELING DATE: 2001-06-11
PRIOR PELING DATE: 2001-06-12
 313 AGKKYFIDFVARETTCSKESNBELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 372
 253 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 312
 61 AGKKYFIDFVARETTCSKESNEELTESCETKKLGQSLDCNAEVYVVPWEKKIYPTVNCQP 120
 9
 Gaps
 PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.
ROMBER OF SEQ ID NOS: 201
LENGTH: 644
TYPE: PT
ORGANISM: Homo sapiens
US-10-162-335-74
 °
 Length 644;
 Indels
 Query Match 100.0%; Score 660; DB 15; Best Local Similarity 100.0%; Pred. No. 5.7e-64; Matches 123; Conservative 0; Mismatches 0;
 Sequence 84, Application US/10162335 Publication No. US20040009480A1 GENERAL INFORMATION:
 APPLICANT: Anderson, David W. APPLICANT: Baldog, Ferenc L. APPLICANT: Boldog, Ferenc L. APPLICANT: Casman, Stacie J. APPLICANT: Edinger, Shlomit R. APPLICANT: Edinger, Shlomit R. APPLICANT: Gangolli, Esha A. APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Hjalt, Tord APPLICANT: Kekuda, Ramesh
 MacDougall, John R.
Malyankar, Uriel M.
Millet, Isabelle
Padigaru, Muralidhara
Patturajan, Meera
Pena, Carol B. A.
Rastelli, Luca
Shimkets, Richard A.
Stone, David J.
 121 LGM 123
 111
373 LGM 375
 RESULT 6
US-10-162-335-84
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69 FVARETTCSKESNEELTESCE---TKKLGQSLDCNAEVYVVPWEKKIYPTVN--CQPLGM 123
 9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID
 10;
 49; Indels
 25.1%; Score 165.5; DB 14; 32.5%; Pred. No. 3.9e-10; iive 22; Mismatches 50;
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
IENGTH: 178 amino acids
TYPE: amino acids
 Query Match

25.6%; Score 169; DB 9;
Best Local Similarity 32.5%; Pred. No. 2.1e-10;
Matches 39; Conservative 22; Mismatches 49
 GENEKAL INFOUNDATION:

GENEKAL INFOUNDATION:

TITLE OF INVENTION: Human Cystatin F
FILE REFERENCE: PF265F1D2

CURRENT APPLICATION NUMBER: US/10/329,428

CURRENT FILING DATE: 2002-12-27

PRIOR APPLICATION NUMBER: 06/014,795

PRIOR FILING DATE: 1996-04-03

PRIOR FILING DATE: 1996-04-03

PRIOR FILING DATE: 1997-04-03

PRIOR FILING DATE: 1997-04-03

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

NUMBER OF SEC ID NOS: 16

SEQ ID NO 2

LENGTH: 145
 CLONE: 30443
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 Sequence 2, Application US/10329428 Publication No. US20030114646A1 GENERAL INFORMATION:
 STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
 Query Match
Best Local Similarity 32.54
Matches 37; Conservative
 ORGANISM: Homo sapiens
US-10-329-428-2
 US-10-329-428-2
 US-09-969-834-1
 RESULT 11
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 d
 252 GDDLFELLPKYCKGCPREIPVDSPELKEALGHSIAQLNAQHNHIFYFKIDTVKKATSQVV 311
 312 AGVIYVIEFIARETNCSKQSKTELTADCETKHLGQSLNCNANVYMRPWENKVVPTVRCQA 371
 1 GKDFVQPPTKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVV 60
 60.8%; Score 401; DB 14; Length 430; 61.8%; Pred. No. 1.5e-35;
 Sequence 215, Application US/10316253
; Publication No. US2003016270641
; GENERAL INPORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: The Procter & Gamble Company
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
LENGTH: 430
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,834
FILING DATE: 01-Oct-2001
CLASSIFTATION: <UNKnown>
 AL INFCRMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
PROTEIN
 CORRESPONDENCE ADRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
 14; Mismatches
 FILING DATE: «Unknown»
PPLICALION NUMBER: US/08/791,522
PILING DATE: «Unknown»
APPLICATION NUMBER: 09/471,765
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/471,765
 Sequence 1, Application US/09969834 Patent No. US20020102711A1 GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-215
 Best Local Similarity 61.8
Matches 76; Conservative
 USA
 COUNTRY:
 121 LGM 123
 372 LDM 374
 61
 Query Match
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9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 68 91 Gaps 69 FVARETICSKESNEELTESCE---TKKLGOSLDCNAEVYVVPWEKKI-YPTVNC 118 VEIGRITCKKNQHLRL-DDCDFQINHTLKQTLSCYSEWWVPWLQHFEVPVLRC 144 .. .. DB 14; Length 145; US-09-746-783-197

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US-09-775-932-12;
Sequence 12, Application US/09775932
Fatent No. US20020137671A1;
GENERAL INFORMATION:
 Sequence 2, Application US/09940497
Patent No. US20020052476Al
GENERAL INFORMATION:
PRIOR FILING DATE: 1998-08-05
 NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin.Ver. 2.0
SEQ ID NO 14
LENGTH: 121
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-775-932-12
 TYPE: PRT
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 34; Conserv
 Query Match
Best Local Similarity
Matches 34; Conserv
 US-09-775-932-14
 US-09-940-497-2
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 54 SRVKPGFPKTIKTNDPGVLQAARYSVEKFNNCTNDMFLFKESRITRALVQIVKGLKYMLE 113
 9 TKICVGCPRDIPTNSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFID 68
 Gaps
 69 FVARETICSKESNEELIESCE---TKKLGQSLDCNAEVYVVPWEKKI-YPTVNC 118
 114 VEIGRTTCKKNOHLRL-DDCDFQTNHTLKÖTLSCYSEVWVVPWLQHFEVPVIRC 166
 5;
 Treacy, Maurice
Spanlading, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
 APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE OF INVENTION: Production and use of Modified Cystatins
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
PRIOR APPLICATION NUMBER: CAS99/00717
PRIOR FILING DATE: 1999-08-05
PRIOR PLING DATE: 1999-08-05
 50; Indels
 COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 DB 10;
 25.1%; Score 165.5; DB 1
32.5%; Pred. No. 4.7e-10;
tive 22; Mismatches 50
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
APPLING DATE: 21-Dec-2000
CLASSIFICATION: «UNKNOWN»
 | LENGTH: 167 anino acids | LENGTH: 167 anino acids | TYPE: anino acid | STRANDEDNESS: «Unknown» | TOPOLOGY: linear | MOLECULE TYPE: procein | SEQUENCE DESCRIPTION: SEQ ID NO: 197: US-09-746-783-197
 NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPRAK: (617) 227-740
INFORMATION POR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
Sequence 197, Application US/09746783
Publication No. USZ0030044935A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
 McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
 Sequence 14, Application US/09775932
Patent No. US20020137671A1
 ATTORNEY/AGENT INFORMATION:
 Query Match
Best Local Similarity 32.5'
Matches 37; Conservative
 NUMBER OF SEQUENCES:
 Cambridge
 GENERAL INFORMATION:
 RESULT 12
US-09-775-932-14
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8 PIKICYGCPRDIPINSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFI 67
 2 PQERMYGELRDLSPDDPQVQKAAQAAVASYNMGSNSIYYFRDTHIIKAQSQLVAGIKYFL 61
 8 PIKICVGCPRDIPINSPELEETLIHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFI 67
 Gaps
 APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: CA99/00717
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 128
 ch 21.0%; Score 138.5; DB 9; Length 128; I Similarity 31.5%; Pred. No. 3.2e-07; 34; Conservative 22; Mismatches 45; Indels 7
 69 IMEMGSTDCRKTRVTGDHVDLT-TCPLAAGAQQEKLRCDFEVLVVPWQ 115
 68 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 109
 68 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 109
th 21.0%; Score 138.5; DB 9; Length Similarity 31.5%; Pred. No. 3e-07; 34; Conservative 22; Mismatches 45; Indels
 PAPELICANT: Ni et al.

TITLE OF INVENTION: Human Cystatin E
FILE REFERENCE: PF202P102
CURRENT APPLICATION NUMBER: US/09/940,497
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/241,376
PRIOR PILING DATE: 1999-02-02
PRIOR PILING DATE: 1996-01-05
PRIOR PILING DATE: 1996-01-05
PRIOR PILING DATE: 1996-01-05
PRIOR PILING DATE: 1995-06-05
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8 PTKICVGCPRDIPTNSPELESTLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFI 67
 30 PQERMVGELRDLSPDDPQVQXAAQAAVASYNMGSNSIYYFRDTHIIXAQSQLVAGIXYFL 89
 22 NSPELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDFVARETICSKESN 81
 Gaps
 Query Match 21.0%; Score 138.5; DB 9; Length 149; Best Local Similarity 31.5%; Pred. No. 3.9e-07; Matches 34; Conservative 22; Mismatches 45; Indels 7;
 90 IMEMGSIDCRKIRVIGDHVDLI-ICPLAAGAQQEKLRCDFEVLVVPWQ 136
 68 DFVARETICSKE----SNEELTESCETKKLGQ--SLDCNAEVYVVPWE 109
 th 20.6%; Score 136; DB 8; Length 112; Similarity 30.6%; Pred. No. 5.1e-07; 34; Conservative 22; Mismatches 31; Indels
 45; Indels
 APPLICANT: Atkinson, Howard J.
APPLICANT: McPherson, Michael J.
APPLICANT: Urwin, Peter E.
TITLE OF INVENTION: MODIFIED PROTEINASE INHIBITORS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSE: All Hackensack
STREET: Hackensack
STREET: New Jersey
COUNTRY: UGA
ZIP: 07601
 CALLY UNFOLL
CALLY UNFOLL
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Elm PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NORMER: US/08/849,303
FILING DATE: 21-MAY-1997
CLESSIFICATION NORMER: US/08/849,303
FILING DATE: 21-MAY-1997
CLESSIFICATION NUMBER: 134
ATTORNEY/AGENT INFORMATION:
NAME: 201-341-1684
TELEFONMULICATION INFORMATION:
TELEFONDE 201-343-1684
TELEFAX: 201-343-1684
TELEX: 13351
INFORMATION FOR SED ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
 Sequence 16, Application US/08849303
Publication No. US20030221209A1
GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
CREANISM: HOMO Sapiens
US-09-940-497-2
 single
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 Query Match
Best Local Similarity
 linear
 STRANDEDNESS:
TOPOLOGY: lir
 US-08-849-303-16
 US-08-849-303-16
 Matches
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Search completed: September 24, 2004, 14:13:03 Job time : 49.296 secs

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